

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2001, 14:04:33 ; Search time 2493.36 Seconds
(without alignments)
11056.979 Million cell updates/sec

Title: US-09-524-101-1
Perfect score: 1573
Sequence: 1 aaatcaaaatagtcggtgg.....agagtgcattattgcaa 1573

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 17159718 seqs, 8763200856 residues

Total number of hits satisfying chosen parameters: 34319436

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_Main:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1573	100.0	1573	1	PCT-US00-06602-1
2	1573	100.0	1573	1	PCT-US00-06602A-1
3	1573	100.0	1573	16	US-09-268-969-1
4	1573	100.0	1573	19	US-09-524-101-1
5	1230	78.2	1241	49	US-60-167-217-22997
6	1230	78.2	1241	50	US-60-171-625-449
7	1230	78.2	1241	50	US-60-173-464-18652
8	1230	78.2	1241	52	US-60-191-637-22729
9	1230	78.2	1241	52	US-60-191-681-17941
10	1067	67.8	5453	49	US-60-167-217-22996
11	1067	67.8	5453	50	US-60-171-625-448
12	1067	67.8	5453	50	US-60-173-464-18651
13	1067	67.8	5454	52	US-60-191-637-22728
14	1067	67.8	5454	52	US-60-191-681-17940
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22	48.2	3.1	15822	24	US-09-620-392-2570
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24	47.2	3.0	7218	16	US-08-466-194-14
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26	41.6	2.6	1530	16	US-09-252-991A-10723
27	41.6	2.6	1704	16	US-09-252-991A-10443
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33	39.4	2.5	257	32	US-09-923-876-2891
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38	39	2.5	439	54	US-60-217-080-25630
39	39	2.5	612	16	US-09-270-849B-16609
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; APPLICANT: EXELIXIS, INC
; TITLE OF INVENTION: Insect p53 Tumor Suppressor Genes and Proteins
; FILE REFERENCE: Insect p53 sequences
; CURRENT APPLICATION NUMBER: PCT/US00/06602A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: EX99-001
; PRIOR FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1573
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
PCT-US00-06602A-1

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Query Match	100.0%; Score 1573; DB 1; Length 1573;
Best local Similarity	100.0%; Pred. No. 0;
Matches 1573; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
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Db 1	aaatccaaatagtcggtggccactaacgattctagttttttgttagcgaattttaat 60
Qy 61	atttagcctcttcccacaagatgcgttgatcagatatagccgaactaatatata 120
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precipitate

RESULTS
UIS-09-268-969-1

03-03-208-509-I
: Sequence 1. Application US/09268969

; GENERAL INFORMATION:

APPLICANT: Buchman, Andrew R.

; APPLICANT: platt, Darren M.

APPLICANT: Ollmann, Michael M.

APPLICANT: Young, Lynn M.

; APPLICANT: Demsky, Madelyn R.

APPLICANT: Keegan, Kevin P.

; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF D. MELANOCASTER TUMOR

; TITLE OF INVENTION: SUPPRESSOR GENES AND USES THEREOF

; FILE REFERENCE: 7326-084

; CURRENT APPLICATION NUMBER: US/

; CURRENT FILING DATE: 199

; NUMBER OF SEQ ID NOS: 27

; SEQ ID NO 1
; LENGTH: 1573
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (112)..(1266)
US-09-268-969-1

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Matches 1573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-09-524-101-1
; Sequence 1, Application US/09524101
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: Insect p53 Tumor Suppressor Genes and Proteins
; FILE REFERENCE: Insect p53 EX00-015
; CURRENT APPLICATION NUMBER: US/09/524,101
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 09/268,969
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/184,373
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1573
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-524-101-1

Query Match 100.0%; Score 1573; DB 19; Length 1573;

RESULT 8

US-60-191-637-22729
; Sequence 22729, Application US/60191637
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: NUCLEIC ACID DETECTION KITS COMPRISING
; TITLE OF INVENTION: GENE SEQUENCES EXPRESSED FROM THE DROSOPHILA GENOME, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000392
; CURRENT APPLICATION NUMBER: US/60/191,637
; NUMBER OF SEQ ID NOS: 2000-03-23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22729
; LENGTH: 1241
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-60-191-637-22729

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 77 caacaaagatcgcttgatcgatagatagccgactaaagatgtatatatacagccaatgtcgt 136
Db 61 caacaaagatcgcttgatcgatagatagccgactaaagatgtatatatacagccaatgtcgt 120
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Db 121 ggcacaaagaaacactgattccgaggaatgactccacgaggtgcgatatcaaggaggata 180
QY 197 ttccgaaacggtggaggatcggaattgaccacggaacccatggcctctttgc 256
Db 181 ttccgaaacggtggaggatcggaattgaccacggaacccatggcctctttgc 240
QY 257 agggattaaactcgggaatctgtagtgcagttcagccagcaaatcgtgctgcgcgaaatga 316
Db 241 agggattaaactcgggaatctgtagtgcagttcagccagcaaatcgtgctgcgcgaaatga 300
QY 317 tgcacagacattcagatccagcggaacacgctgcgccaagctagagaatacaacatcg 376
Db 301 tgcacagacattcagatccagcggaacacgctgcgccaagctagagaatacaacatcg 360
QY 377 gtggtattgttcagatggttctggatgagccgccaagtcctttgtgattgactcga 436
Db 361 gtggtattgttcagatggttctggatgagccgccaagtcctttgtgattgactcga 420
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Db 421 ttccgctgaacaagctctacatccgagatgaacaaaggccctcaacggttcagttca 480
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Db 481 agtcaaaatgccatcccaaccacttaatttgctgtgttctttcttccatgatg 540
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RESULT 9

US-60-191-681-17941
; Sequence 17941, Application US/60191681
; GENERAL INFORMATION:
; APPLICANT: Li, Peter, W.D.
; TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING ISOLATED DROSOPHILA PROTEINS AND
; TITLE OF INVENTION: USES THEREOF.
; FILE REFERENCE: cl000390
; CURRENT APPLICATION NUMBER: US/60/191,681
; CURRENT FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 30973
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17941
; LENGTH: 1241
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-60-191-681-17941

Query Match 78.2%; Score 1230; DB 52; Length 1241;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 77 caacaaagatcgcttgatcgatagatagccgactaaagatgtatatatacagccaatgtcgt 136
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Db 121 ggcacaaagaaacactgattccgaggaatgactccacgaggtgcgatatcaaggaggata 180

QY 197 ttccgaaacggtggaggatcggaattgaccacggaacccatggcctcttgc 256
Db 181 ttccgaaacggtggaggatcggaattgaccacggaacccatggcctcttgc 240
QY 257 agggattaaactccgggaatctgagttccagcagcaatccgtgctgcgcaaatga 316
Db 241 agggattaaactccgggaatctgagttccagcagcaatccgtgctgcgcaaatga 300
QY 317 tgcgcaggacatccagtcagcagcgaacacgctgccagctagagatcacacacatcg 376
Db 301 tgcgcaggacatccagtcagcagcgaacacgctgccagctagagatcacacacatcg 360
QY 377 gtgattattcttcagctggttggatgagccgccagtcctcttggatgtaactcga 436
Db 361 gtgattattcttcagctggttggatgagccgccagtcctcttggatgtaactcga 420
QY 437 ttccgctgaacagctctacatccagatgaacaggccttcaacgtgagcttcaagtcca 496
Db 421 ttccgctgaacagctctacatccagatgaacaggccttcaacgtgagcttcaagtcca 480
QY 497 agtctaaatgccatccacacacttaattggctggtgttcttcttcttccaatgatg 556
Db 481 agtctaaatgccatccacacacttaattggctggtgttcttcttcttccaatgatg 540
QY 557 tgagtgctcccggtggtccgctgtcaaaatccacttagcttgagcctttgacggccaata 616
Db 541 tgagtgctcccggtggtccgctgtcaaaatccacttagcttgagcctttgacggccaata 600
QY 617 acgcaaaaatgcgcgagagctgtgcgcagcagagaaatcccaacagctgtatatgtggaa 676
Db 601 acgcaaaaatgcgcgagagctgtgcgcagcagagaaatcccaacagctgtatatgtggaa 660
QY 677 atgctcaggcgaaggaaatccgagcgttttccgtgtgtagtcccccctgaacatgagcc 736
Db 661 atgctcaggcgaaggaaatccgagcgttttccgtgtgtagtcccccctgaacatgagcc 720
QY 737 ggtctgaacccgagtggtgctcagcgcagacccctggccttcaagttctgtcgccaaa 796
Db 721 ggtctgaacccgagtggtgctcagcgcagacccctggccttcaagttctgtcgccaaa 780
QY 797 actcgtatggcggaagaaactccttagtctctctccttgcctggagaaagatcgcgcg 856
Db 781 actcgtatggcggaagaaactccttagtctctctccttgcctggagaaagatcgcgcg 840
QY 857 atatcgtggagacagcatgttatcatgttaaaatattgactgcccacagcgggatcgca 916
Db 841 atatcgtggagacagcatgttatcatgttaaaatattgactgcccacagcgggatcgca 900
QY 917 tccaagacgaacgcagctcaatagcaagaagcgcaagtcctgtjccgggaagccgcgaag 976
Db 901 tccaagacgaacgcagctcaatagcaagaagcgcaagtcctgtjccgggaagccgcgaag 960
QY 977 aagatgaacgcgtccaagtgctcggtgcatgttatataaagacggagacagcgagagca 1036
Db 961 aagatgaacgcgtccaagtgctcggtgcatgttatataaagacggagacagcgagagca 1020
QY 1037 atgatacgagactgcgacagctccgcgcagagtggaacgtgtcgcgggacacacgggatg 1096
Db 1021 atgatacgagactgcgacagctccgcgcagagtggaacgtgtcgcgggacacacgggatg 1080
QY 1097 gogattaccgtctggtattacgtgcccataaagggaatggctgtcgcagag atcgagg 1156
Db 1081 gogattaccgtctggtattacgtgcccataaagggaatggctgtcgcagag atcgagg 1140
QY 1157 gcatgattaaaggcgcggtgaagtctcgtcgcaatcccaacacgaagagaatctacgtc 1216
Db 1141 gcatgattaaaggcgcggtgaagtctcgtcgcaatcccaacacgaagagaatctacgtc 1200
QY 1217 gccatgccaacaaattcagccttaaga 1246
Db 1201 gccatgccaacaaattcagccttaaga 1230

RESULT 10
US-60-167-217-22996
; Sequence 22996, Application US/60167217
; GENERAL INFORMATION:
; APPLICANT: Li, Peter W. D.
; TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING DROSOPHILA PROTEINS, AND USES
; FILE REFERENCE: CL000152
; CURRENT APPLICATION NUMBER: US/60/167,217
; CURRENT FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 23195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22996
; LENGTH: 5453
; TYPE: DNA
; ORGANISM: Drosophila
US-60-167-217-22996

Query Match 67.8%; Score 1067; DB 49; Length 5453;

Best Local Similarity 87.4%; Pred No. 5,1e-297;

Matches 1282; Conservative 0; Mismatches 0; Indels 185; Gaps 3;

QY 292 cagcaatccgtgctgcggaatgatgctgcaggacattccagtcagtcggaacacgctg 351
Db 3362 cagcaatccgtgctgcggaatgatgctgcaggacattccagtcagtcggaacacgctg 3421
QY 352 ccaagctagagaatcaacaacatcgtgttattgtcttcagcatggttctggatgagccg 411
Db 3422 ccaagctagagaatcaacaacatcgtgttattgtcttcagcatggttctggatgagccg 3481
QY 412 ccaagctcttcttgatgactcgttcgctgcagtcggaacagctctacatccggtgaacaag 471
Db 3482 ccaagctcttcttgatgactcgttcgctgcagtcggaacagctctacatccggtgaacaag 3541
QY 472 gcttcaacgtggacgttccagttcaagtctaaatgccatccacacacttaattgct 531
Db 3542 gcttcaacgtggacgttccagttcaagtctaaatgccatccacacacttaattgct 3601
QY 532 ggtctcttctcttcacatgatgagtgctcccgctgctccgctgctcaaaaacactt 591
Db 3602 ggtctcttctcttcacatgatgagtgctcccgctgctccgctgctcaaaaacactt 3661
QY 592 agcgttgagcctt----- 604
Db 3662 agcgttgagccttctgaagtaaacataacagatcgcaacagattatttaactatca 3721
QY 605 -----tgacggccaataacgcgaataatgcgcagagagcttgcgcgag 647
Db 3722 ttgtacaaaactttagtgacgcgcgaataacgcgaataatgcgcagagagcttgcgcgag 3781
QY 648 cgagaatcccaacagctgtatatgtggaatgctcagggcgaagggaatttccgagcgttt 707
Db 3782 cgagaatcccaacagctgtatatgtggaatgctcagggcgaagggaatttccgagcgttt 3841
QY 708 ttccgtgttagtcccccctgaacatgagccggtctgtaaccccagctggttccacgcgcca 767
Db 3842 ttccgtgttagtcccccctgaacatgagccggtctgtaaccccagctggttccacgcgcca 3901
QY 768 gacctggccttcaagttctgtccaaaactcgtgtatcggggcgaagaaacttccct 827
Db 3902 gacctggccttcaagttctgtccaaaactcgtgtatcggggcgaagaaacttccct 3961
QY 828 agtctctcctctggagaaagcat----- 850
Db 3962 agtctctcctctggagaaagcat-----gcgcgatatactgtgggacagcatgttatcatgtt 885
QY 851 -----gcgcgatatactgtgggacagcatgttatcatgtt 4081
Db 4022 agtctaacgttttcttcttgcgcgcatcgtgggacagcatgttatcatgtt 4081
QY 886 aaaaatgtacgtgcccaacgagggatcgcatccaagacgaacgcccagctcaatag-aag 945

4382	ctgcgaatcccaaccacaagaatactacgtgcgcattgcacaaaattgctgagccttaag	4441
1246	a-----	1246
4442	agtaacgagtgaaatcgaggagcaaaagagattaagctttaactaccgaactttcctttcga	4501
1247	aacgtgctcagcagctgcacgaactctctgtatctgctgcacaaatctccaggtatcaagata	1306
4502	aacgtgctcagcagctgcacgaactctctgtatctgctgcacaaatctccaggtatcaagata	4561
1307	cccttgaatactgttgacatctcgtcgggtactacacatagctca: agtactcttaagtttgt	1366
4562	cccttgaatactgttgacatctcgtcgggtactacacatagctca: agtactcttaagtttgt	4621
1367	attagtcctttcttcgtaagcgttttaacgctgatattccctc: tggcatgttcgatggcc	1426
4622	attagtcctttcttcgtaagcgttttaacgctgatattccctc: tggcatgttcgatggcc	4681
1427	cgaaaagaaaacatttttatatttttgatagataactgtttgtaactgcagttctatgtg	1486
4682	cgaaaagaaaacatttttatatttttgatagataactgtttgtaactgcagttctatgtg	4741
1487	actacgttaacttttgtctaccacaacaaacatactctgtacaaaaaagccaaaagtgaat	1546
4742	actacgttaacttttgtctaccacaacaaacatactctgtacaaaaaagccaaaagtgaat	4801
1547	ttattaaagagttgtcatattttgcaa	1573
4802	ttattaaagagttgtcatattttgcaa	4828

```

RESULT 12
US-60-173-464-18651
/ Sequence 18651, Application US/60173464
/ GENERAL INFORMATION:
/ APPLICANT: Li, Peter W.D.
/ TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
/ TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS AND USES
/ TITLE OF INVENTION: THEREOF
/ TITLE OF INVENTION: CL000173
/ FILE REFERENCE: CL000173
/ CURRENT APPLICATION NUMBER: US/60/173,464
/ CURRENT FILING DATE: 1999-12-29
/ NUMBER OF SEQ ID NOS: 30269
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 18651
/ LENGTH: 5453
/ TYPE: DNA
/ ORGANISM: Drosophila
US-60-173-464-18651

```

Query Match	67.8%;	Score 1067;	DB 50;	Length 5453;
Best Local Similarity	87.4%;	Pres. No. 5.1e-297;		
Matches 1282;	Conservative	0;	Mismatches	185; Gaps
Qy	292	cagcaatccctgcgcgcgaaataatgctcagagacattcagatccacggcggaacacgcgtg	351	
Db	3362	cagcaatccctgcgcgcgaaatgatgctcagagacattcagatccacggcggaacacgcgtg	3421	
Qy	352	cccaagctcagagaatcacacacatcgggtggtattgcttcagcatcgtgtcttcggatgagccg	411	
Db	3422	cccaagctcagagaatcacacacatcgggtggtattgcttcagcatcgtgtcttcggatgagccg	3481	
Qy	412	cccaagctcttttggatgtactcgtatgctccgcgcgaacaaagctctacatccggatgaacaag	471	
Db	3482	cccaagctcttttggatgtactcgtatgctccgcgcgaacaaagctctacatccggatgaacaag	3541	
Qy	472	gcttcaacgtggacgttcagttcaagctcctcaaatgccatccacaacacttaatttgcgt	531	
Db	3542	gcttcaacgtggacgttcagttcaagctcctcaaatgccatccacaacacttaatttgcgt	3601	
Qy	532	gtgttcctttgctctcccaatgatgtgagtgctcccggtgctcgtgtccaaatcaactt	591	

Db	3602	gtgttcctttgtcttccaatgatgtgagtgctcccgtagtcccgctgtcaaaatacaacctt	3661
QY	592	agcgtttagacctt----- 	604
Db	3662	agcgtttagccttgttaagtgaagataaacaatacacagatcgacaagattatttaactaca	3721
QY	605	----- -----tgacggccataacgcgcaaaatgcgcgagagcttgcctgcgcag	647
Db	3722	ttttgtacaaacctttagtgcggccaaataacgcgcaaaatgcgcgagagcttgcctgcgcag	3781
QY	648	cgaagaatcccaacagtgatatgtggaattgcttcaggcgaagaaatttccgagcgttt	707
Db	3782	cgaagaatcccaacagtgatatgtggaattgcttcaggcgaagaaatttccgagcgttt	3841
QY	708	ttccgttgtagtcctccctgaacatgagccgtctgttaaccgcagctgggctcacgcgcca	767
Db	3842	ttccgttgtagtcctccctgaacatgagccgtctgttaaccgcagctgggctcacgcgcca	3901
QY	768	gacctggccttaagtctgctgcgaacctctgatacgggcgcaaaagaacttccctt	827
Db	3902	gacctggccttaagtctgctgcgaacctctgatacgggcgcaaaagaacttccctt	3961
QY	828	agttcttctgcctagaagaagcat----- 	850
Db	3962	agttcttctgcctagaagaagcat----- 	4021
QY	851	----- -----gcggcgatatcgtgggacagcatgtatatacatgtt	885
Db	4022	agcttaacgtgtttttcttctgcagcgcgatctgtggacagcatgtatatacatgtt	4081
QY	886	aaatatgtactgtccccaagcgggatcgcatccaagacgaacgcgcagctcaatagcaag	945
Db	4082	aaatatgtactgtccccaagcgggatcgcatccaagacgaacgcgcagctcaatagcaag	4141
QY	946	aagcgcaagt--cgtgcggaagccccaagaagaatgaagccgtccaaggtcgtgcgtgc	1005
Db	4142	aagcgcaagtccgtgcggaagccccaagaagaatgaagccgtccaaggtcgtgcgtgc	4201
QY	1006	attgctataaagacgcggagacgcggagagcaatgatagccgagactgcgaacactccgcc	1065
Db	4202	attgctataaagacgcggagacgcggagagcaatgatagccgagactgcgaacactccgcc	4261
QY	1066	gcagagtgaacactgtcgcggacacccggatggcgattaccgtctggctattacgtgcgcc	1125
Db	4262	gcagagtgaacactgtcgcggacacccggatggcgattaccgtctggctattacgtgcgcc	4321
QY	1126	aataaggaatggctgctgcagagcatcgaaggcgcgtattaaaggagcgcgcgtcgaatgc	1185
Db	4322	aataaggaatggctgctgcagagcatcgaaggcgcgtattaaaggagcgcgcgtcgaatgc	4381
QY	1186	ctgcgcgaatcccaaccaagaagaatctacgtccgcattgcacaataatgctgagccttaag	1245
Db	4382	ctgcgcgaatcccaaccaagaagaatctacgtccgcattgcacaataatgctgagccttaag	4441
QY	1246	a----- -----	1246
Db	4442	agtaagcagtgaaatcggaggacaaagagattaagcttttaacttaacggaaacttcccttcag	4501
QY	1247	aacgtgctctacgagctcccatgactctgatctgctgcgacaatctccaggtatcagata	1306
Db	4502	aacgtgctctacgagctcccatgactctgatctgctgcgacaatctccaggtatcagata	4561
QY	1307	cccttgaatatgttgcattctggggtatacactagctattagattctttaagtttgt	1366
Db	4562	cccttgaatatgttgcattctggggtatacactagctattagattctttaagtttgt	4621
QY	1367	attagtccttctgtcgaagcgtttaacgctgatactcccttttggcatgttcgatggc	1426
Db	4622	attagtccttctgtcgaagcgtttaacgctgatactcccttttggcatgttcgatggc	4681
QY	1427	cgaagaagaacaatttttatattttgtatagttactgttgttaactgcagttctatgtg	1486
Db	4682	cgaagaagaacaatttttatattttgtatagttactgttgttaactgcagttctatgtg	4741

QY 1487 actacgtaacttttctaccacacacatactctgtacacaaagccaaagtgaaat 1546
Db 4742 actacgtaacttttctaccacacacatactctgtacacaaagccaaagtgaaat 4801
QY 1547 ttattaaagagttgcatattttgcaa 1573
Db 4802 ttattaaagagttgcatattttgcaa 4828

RESULT 13

US-60-191-637-22728/c
; Sequence 22728, Application US/60191637
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: NUCLEIC ACID DETECTION KITS COMPRISING
; TITLE OF INVENTION: GENE SEQUENCES EXPRESSED FROM THE DROSOPHILA GENOME, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000392
; CURRENT APPLICATION NUMBER: US/60/191,637
; CURRENT FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 42660
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22728
; LENGTH: 5454
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-60-191-637-22728

Query Match 67.8%; Score 1067; DB 52; Length 5454;
Best Local Similarity 87.4%; Pred. No. 5.1e-297;
Matches 1282; Conservative 0; Mismatches 0; Indels 185; Gaps 3;

QY 292 cagcaatccgtctgcgcgaatactctcagacacattcagatccagcgcaacacgctg 351
Db 2092 CAGCAATCCGTCTGCGGAAATGATGCTGCAGGACATTCAGATCCAGCGCAACCGCTG 2033
QY 352 cccaagctagagaatcacacaatcgctggttattgttcagcatggttcgtgatgagccg 411
Db 2032 CCCAAGCTAGAGAATCACACAATCGCTGTTATTGCTTCAGCATGTTCTGGATGAGCCG 1973
QY 412 cccaagctctcttggtatctactgactccgctgaacaagctctacatccgagatgaacaag 471
Db 1972 CCCAAGCTCTTTGGGATGCTACGCGATTCGCGTGAACAAGCTCAGATCCGGATGAACAAG 1913
QY 472 gcctcaactgagacttcagttcaagttcaagtcaaaatgccatcccaacttaatttcgct 531
Db 1912 GCCTTCACGTGACCGTTTCAGTCAAGTCTAAATGCCCCATCCACCACTTAATTTGCGT 1853
QY 532 gtgttcctttgtctccaatgatgagtgctccgctgctccgctgtccaaatcaactt 591
Db 1852 GTGTTCCTTTGCTCTCCAAATGATGAGTGCTCCCGTGCTCGCTGTCAAAATCACCTT 1793
QY 592 agcgttgagcctt----- 604
Db 1792 AGCGTTGAGCCTTTGTAAGTGAAGATAACAACAGATGCAACAGGATTTATTAACATATCA 1733
QY 605 -----tgacgccaataacgcacaaatgcgcagagcttgctgcgcag 647
Db 1732 TTTGTACAACACCTTTAGTGACCGGCCAATACGCAAAATGCGGAGAGCTTGCTGCGGAG 1673
QY 648 cgagaatcccaacagtgatatatttggaatgctcagggcaatgaatttcgcagcgctt 707
Db 1672 CGAGAATCCCAACAGTGATATTGTGGAATGCTCAGGCAACAGGAATTTCCGAGCGTTT 1613
QY 708 ttccgttgtagtcccttgaacatagccgctgtctgaaccgcagtggtgctcaagcgcca 767
Db 1612 TTCCGTTGTTAGTCCCTTGAACATGAGCGGCTGTCAACCGCAGTGGCTCACGCGCCA 1553
QY 768 gacctggccttaagttcgtctgcacaaactcgtgatcggcgcaaaagaacttcctt 827
Db 1552 GACCGTGCCTTCAAGTGTGTCGCAAACTCGTGTATCGGCGCAAAAGAACTTCCTT 1493

QY 828 agtcttctgctggaaagcat----- 850
Db 1492 AGTCTTCTGCTGGAGAAAGCATGTAAGGTGACAGCAAACTCTAGATGGCTAGAACAA 1433
QY 851 -----ggcgcatatcgtggacagcatgtt..acatgtt 885
Db 1432 AGCTTAACGTGTTTTCTTTCTTCAGCGCGCATATCTGGGACAGATGTTATACATGTT 1373
QY 886 aaaatatgtacgtgcccccaagcgggatcgcatccaagacgaacgcgcagctcaatagcaag 945
Db 1372 AAAATATGTACGTGCCCCCAAGCGGGATCGCATCCAGACGACGCCAGCTCAATAGCAAG 1313
QY 946 aagcgcaagtcctgctgcggaagcccccgaagaagatgagccgtcccaagtgctcggtgc 1005
Db 1312 AAGCGCAAGTCCGTGCGGAAGCCCGCAAGATGAGCGCTCCCAAGGTGCTGCGGTGC 1253
QY 1006 attgctataaagacgagagacgagagacgaatgtagccgagagatgcgagactccgccc 1065
Db 1252 ATTGCTATAAAGACGGAGGACACGCGAGAGCAATGATAGCCGAGACTGCGAGACTCCGCC 1193
QY 1066 gcagagtggaacgtgctgcgcgacaccgcatggtacgttaccgtctgctgcttattacgtgcccc 1125
Db 1192 GCAGAGTGGAAAGTGTGCGGGACACCGGATGCCGATTACCGTCTGGCTATTACGTGCCCC 1133
QY 1126 aataaggaatggctgctgcagagcatcgagggcatgattaagagagcgcgctgaagtc 1185
Db 1132 AATAAGGAATGGCTGCTGCAGAGCATCGAGGGCATGATTAAAGAGCGCGCGCTGAAGTC 1073
QY 1186 ctgcgcaatcccaacaaagagaatctacgtcgccatgcacaaataatgctgagccttaag 1245
Db 1072 CTGCGCAATCCCAACCAAGAGAATCTACGTGCGCATCCCAAAATTTGCTGAGCCTTAAG 1013
QY 1246 a----- 1246
Db 1012 AGTAAGACGTAATCGGAGGACAAAGAGATTAAAGCTTTACTTACCGAACTTTCTTTTCAG 953
QY 1247 aacgtgctacagagctgccatcactctgctgctgcacaatctcccaggtatcagata 1306
Db 952 AACGTGCTACGAGCTGCCATGACTTCTGATCTGCTGTCGCAAACTCCCAAGGTATCAGATA 893
QY 1307 cctttgaaatggttgcatctgtgggtatatactacatagctattagattcttaagttgt 1366
Db 892 CCTTTGAAATGTTGTCATCTGTGGGTATATCATAGCTATTAGTATCTTTAAGTTTGT 833
QY 1367 attagtcctgttcgttaagcgcttcaacggtgatctcccttttgcattgctcagtcgc 1426
Db 832 ATTAGTCTCTTTCGTAAGCGTTTAAAGGTGATATCCCGTTTGGCATGTCGATGGC 773
QY 1427 cgaaagaaaacatttttatattttgtagtagtactgtttgtaactgcagttctatgtg 1486
Db 772 CGAAAGAAACAACTTTTATATTTTGTATAGTATAGTATGTTGTTAACTGCAGTTCTATGTG 713
QY 1487 actaagtaactttgtctaccacaaacatactctgtacacaaagccaaagtgaaat 1546
Db 712 ACTAGTAACCTTTTGTCTACCAACAACACTACTCTGTACAAAAAGCCAAAAAGTGAAT 653
QY 1547 ttattaaagagttgcatattttgcaa 1573
Db 652 TTATTAAAGAGTTGTCATATTGTCAA 626

RESULT 14

US-60-191-681-17940/c
; Sequence 17940, Application US/60191681
; GENERAL INFORMATION:
; APPLICANT: Li, Peter, W.D.
; TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING ISOLATED DROSOPHILA PROTEINS AND
; TITLE OF INVENTION: USES THEREOF.
; FILE REFERENCE: cl000390
; CURRENT APPLICATION NUMBER: US/60/191,681
; CURRENT FILING DATE: 2000-03-23

NUMBER OF SEQ ID NOS: 30973
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 17940
LENGTH: 5454
TYPE: DNA
ORGANISM: DROSOPHILA
US-60-191-681-17940

Query Match 67.8%; Score 1067; DB 52; Length 5454;
Best Local Similarity 87.4%; Pred. No. 5.1e-297;
Matches 1282; Conservative 0; Mismatches 0; Indels 185; Gaps 3;

QY 292 cagcaatccgtgctgcgcgaatgatcgatcgagacattcagatccagcgcaacacgctg 351
|||||
Db 2092 CAGCAATCCGTGCTGCGGAATGATGCTCAGGACATTCAGATCCAGCGCAACGCTG 2033
|||||
QY 352 cccaagctagagaatcacacaatcgtggtattgcttcagcatggtctcgatgagccg 411
|||||
Db 2032 CCCAAGCTAGAGAATCACAAATCGTGGTTATTGCTTCAGCATGGTCTGGATGAGCG 1973
|||||
QY 412 cccaagctctttggatgactgattccgcgaacagctcacaatccogtatgaacaag 471
|||||
Db 1972 CCCAAGCTCTTTGGATGACTCGATTCGCTGAACAAGCTCTACATCCGGATGAACAAG 1913
|||||
QY 472 gcttcaacgtgacattcagttcaagtctaaatgccatcccaacccttaatttcgt 531
|||||
Db 1912 GCCTTCACGTGACGCTTCAGTTCAGGCTAAATGCGCCATCCCAACCTTAAATTCGGT 1953
|||||
QY 532 gtgttccttcttcccaatgatgtagtgcctccggtgcgtgcgtgcgtgcgaataccctt 591
|||||
Db 1852 GTGTTCCTTTCTTCCATGATGTGAGTGTCTCCGCTGGCTGTCCAAATCACCTT 1793
|||||
QY 592 agcgttagcctt----- 604
|||||
Db 1792 AGCCTTGAGCCTTTGAAGTGAAGATAACAATACAGATCGAACAGGATTATTTAACTATCA 1733
|||||
QY 605 -----taacgccaataacgcgaataatcgagagcttgcgcgag 647
|||||
Db 1732 TTGTACAAACCTTTAGTGAGCGCCAAATACGCAAAATCGCGAGAGCTTCTCGCGAG 1673
|||||
QY 648 cgagaatcccaacagtgatatttggaaatgctcaggcgcaagggaattcccgagcgttt 707
|||||
Db 1672 CGAGAATCCCAACAGTATATTGTGGAAATGCTCAGGCGCAAGGAAATTCOGAGCGTT 1613
|||||
QY 708 ttccgtgtgattccctgaacatagcgcgtctgttaacccgagtggtgcacgcga 767
|||||
Db 1612 TTCCGTTGTAGTCCCTGAAACATGAGCGGCTGTGTAACCCCGAGTGGCTCACGCGCA 1553
|||||
QY 768 gacctgacctcaagttcgtctgcgaactcgtgtagcggaagaaacttcctt 827
|||||
Db 1552 GACCTGCGCTTCAAGTTCTGTGCGCAAACTGTGTATCGGCGGAAAGAACTTCCTT 1493
|||||
QY 828 agtcttctgctgagaaagcat----- 850
|||||
Db 1492 AGTCTTCTGCTGGAGAAAGCATGTGTAAGTGCAGCAAAACCTAGATGGCTAGACAA 1433
|||||
QY 851 -----gcggcgatatcgtgggacagcatgttatcatgtt 885
|||||
Db 1432 AGCTTAAGCTGTTTTCTTTCTTCAGCGCGCATATCTGGGACAGCATGTTATCATGTT 1373
|||||
QY 886 aaaaatatagtcgccccagcgagatcgatccaaagcaaacgacagctcaatagaag 945
|||||
Db 1372 AAAATATAGTCCCTCAAGCGGGATCGATPCCAAAGCAACGCCAGCTCAATAGCAAG 1313
|||||
QY 946 aagcgcaagtcgtgcgcgaagcgccgaagaagatgagcgtcccaaggtgcgtcggtgc 1005
|||||
Db 1312 AAGCGCAAGTCCGTGCGCGAAGCGCGCAAGAGATGAGCGCTCCAGAGTGGCTGCTGTC 1253
|||||
QY 1006 attgctataaagacggaggacacgagagcaatgatagccgagactgcacgaactccgcc 1065
|||||
Db 1252 ATTGTATAAAGACGGAGACACGGAGAGCAATGATAGCCGAGACTGCCAGACTCCGCC 1193
|||||

QY 1066 gcagagtgaacgtgtgcgcgacacccgagatggcgattacccgtctggtctattacgtgcctc 1125
|||||
Db 1192 GCAGAGTGAACGTGTGCGGACACCGGATGGCGATTACCGTCTGCTGCTATACGTGCC 1133
|||||
QY 1126 aataaggaaatgctgcgcgagcatcgagggcatgattaaaggagcgcgctgaagtc 1185
|||||
Db 1132 AATAAGGAATGGCTGCTGCGAGAGCATCGAGGCGCATGATTAAAGGAGCGCGCTGAAGTC 1073
|||||
QY 1186 ctgcgaatcccaacaaagagaatctagtcgccaatgccaaacaaatgctgagccttaag 1245
|||||
Db 1072 CTGCGCAATCCCAACCAAGAAATCTACGTGCGCATGCCAACAAATGCTGAGCCTTAAG 1013
|||||
QY 1246 a----- 1246
|||||
Db 1012 AGTAGCAGTGAATCGGAGCACAAAGAGATTAAAGCTTTACTTTACCGAACTTTCTTTTTCAG 953
|||||
QY 1247 aacgtgctacgagtcgcatcctgactctgtgtgtgcgaatctccacaggtatcagata 1306
|||||
Db 952 AACGTGCCCTAGAGTCGCCATGACTTCTGATCTGTCGACAATCTCCAGGTATCAGATA 893
|||||
QY 1307 cctttgaaatgtgtgcatctggtgggtatactactacatagctattagttatcttaagtgt 1366
|||||
Db 892 CCTTTGAAATGTGTGATCTGTGGGTATCTACATAGCTATTAGTATCTTAAAGTTGT 833
|||||
QY 1367 attagtcctgttcgtaagcggtttaacggtgatattcccttttggcatgttcgatgac 1426
|||||
Db 832 ATTAGTCTTGTTCGTAAAGCGGTTTAAACGTGATATCCCTTTTGGCATGTCATGGC 773
|||||
QY 1427 cgaagaagaaacatttttatatttttgatagtagtactgtgttaactgcagttctatgt 1486
|||||
Db 772 CGAAAAGAAAACATTTTATATTTTTGTATGATATACTGTTGTTAACTGCCAGTTCTATGTG 713
|||||
QY 1487 actagtgaaactttgtctacacacaaacataactctacaaaaagccaaagtgaat 1546
|||||
Db 712 ACTAGCTAACCTTTTGTACCAACAAACATACTCTGTACAAAAAGCCAAAAAGTGAAT 653
|||||
QY 1547 ttattaaagagttgctatattttgcaa 1573
|||||
Db 652 TTATTAAAGAGTTGTCATATTTTGCRA 626
|||||

RESULT 15
US-09-268-969-7
; Sequence 7, Application US/09268969
; GENERAL INFORMATION:
; APPLICANT: Buchman, Andrew R.
; APPLICANT: Platt, Darren M.
; APPLICANT: Ollmann, Michael M.
; APPLICANT: Young, Lynn M.
; APPLICANT: Demsky, Madelyn R.
; APPLICANT: Keegan, Kevin P.
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF D. MELANOGASTER TUMOR
; FILE REFERENCE: 7326-084
; CURRENT APPLICATION NUMBER: US/09/268,969
; CURRENT FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 7
; LENGTH: 8805
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-268-969-7

Query Match 67.8%; Score 1067; DB 16; Length 8805;
Best Local Similarity 87.4%; Pred. No. 6.4e-297;
Matches 1282; Conservative 0; Mismatches 0; Indels 185; Gaps 3;

QY 292 cagcaatccgtgctgcgcgaatgatcgatcgagacattcagatccagcgcaacacgctg 351
|||||
Db 3599 cagcaatccgtgctgcgcgaatgatcgatcgagacattcagatccagcgcaacacgctg 3658
|||||

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QY 352 ccaagctagagaatcaacacatcggtggttattgtctcagcatggtcttgatgagccg 411
|||||
Db 3659 ccaagctagagaatcaacacatcggtggttattgtctcagcatggtcttgatgagccg 3718
QY 412 ccaagctcttttgatgatactcgatccgctgaacacagctctacatcccgatgaacaag 471
|||||
Db 3719 ccaagctcttttgatgatactcgatccgctgaacacagctctacatcccgatgaacaag 3778
QY 472 gcttcaacgtagagcttcagttcaagtctaaatgccatcccaacacacttaatttgcgt 531
|||||
Db 3779 gcttcaacgtagagcttcagttcaagtctaaatgccatcccaacacacttaatttgcgt 3838
QY 532 gtgtctctttgtcttccaaatgatgtgagtgctcccggtcccgctgtcgaataatccctt 591
|||||
Db 3839 gtgtctctttgtcttccaaatgatgtgagtgctcccggtcccgctgtcgaataatccctt 3898
QY 592 agcgttgagccct----- 604
|||||
Db 3899 agcgttgagcccttgaagtgaagataacaatacacagatcgaaacagattatttaactatca 3958
QY 605 -----tgacgcccataaagcgaataatgcgcgagagcttgcgtgcgacg 647
|||||
Db 3959 ttgtacaaacaccttagtgacgcccataaagcgaataatgcgcgagagcttgcgtgcgacg 4018
QY 648 cgagaatcccaacagtgatatatttggaatgtctcggggcgaagggaatttccgagcgctt 707
|||||
Db 4019 cgagaatcccaacagtgatatatttggaatgtctcggggcgaagggaatttccgagcgctt 4078
QY 708 ttcggttgtagtcccttgaaacatgagccggtctgttaaccccgagtgaggtcacgcgcca 767
|||||
Db 4079 ttcggttgtagtcccttgaaacatgagccggtctgttaaccccgagtgaggtcacgcgcca 4138
QY 768 gacctgagcttcaagttcgtctgcgaatactcgtgtatcgggcgaagaaagaaacttccct 827
|||||
Db 4139 gacctgagcttcaagttcgtctgcgaatactcgtgtatcgggcgaagaaagaaacttccct 4198
QY 828 agtctctgctggagaagacat----- 850
|||||
Db 4199 agtctctgctggagaagacatgtaaggtgacagcaaaactctatagtggtagaacaa 4258
QY 851 -----ggcgcatatcgtgggacagcatgttatcatgtt 885
|||||
Db 4259 agcttaacgtgttttcttcttgcggcggtatcgtgggacagcatgttatcatgtt 4318
QY 886 aaaatatgtacgtgccccgaagcgggacatcccaagcagcaacgcgcagctcaatagcaag 945
|||||
Db 4319 aaaatatgtacgtgccccgaagcgggacatcccaagcagcaacgcgcagctcaatagcaag 4378
QY 946 aagcgcaagtccgtgcccgaagccgcgaagaagatgagccgtccaaaggtgcgtgcgtgc 1005
|||||
Db 4379 aagcgcaagtccgtgcccgaagccgcgaagaagatgagccgtccaaaggtgcgtgcgtgc 4438
QY 1006 attgctataaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1065
|||||
Db 4439 attgctataaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 4498
QY 1066 gcagagtggaacgtgctgcgggacacgcgagtgccgattacccgtctggtctattacgtgcgcc 1125
|||||
Db 4499 gcagagtggaacgtgctgcgggacacgcgagtgccgattacccgtctggtctattacgtgcgcc 4558
QY 1126 aataaggaatggctgctgcagagcagcagcagcagcagcagcagcagcagcagcagcagc 1185
|||||
Db 4559 aataaggaatggctgctgcagagcagcagcagcagcagcagcagcagcagcagcagcagc 4618
QY 1186 ctgcgcaatcccaacaaagaatactacgtcgcgcacatgcgaataatgcgtgagccttaag 1245
|||||
Db 4619 ctgcgcaatcccaacaaagaatactacgtcgcgcacatgcgaataatgcgtgagccttaag 4678
QY 1246 a----- 1246
|||||
Db 4679 agtaagcagtgaaatcgaggagcaagaagagattaaagctttaactaccgaacttcccttcag 4738
QY 1247 aacgtgctacagctgcgatgactctgatctgtgtgcacaatctcccgaggtatcagata 1306
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Search completed: November 16, 2001, 15:47:04
Job time: 6151 sec

[illegible]

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RESULT      9
US-09-815-242-4152
US-09-815-242-4152, Application US/09815242
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011a
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4152
; LENGTH: 1320
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-815-242-4152

```

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Query Match      2.2%; Score 34.2; DB 5; Length 320;  
Best Local Similarity   67.6%; Pred.No. 7.2;  
Matches 48; Conservative    0; Mismatches     23; Indels       0; Gaps        0;
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Qy	426 gatgtactgattccgctgaacaaagcctcatatocgggatgaacaaggccttcaacgtgga
Dd	69 gctgtttccaaggcgctaaccctggtctacctgctgatgaacgaggacgi.gatcgc tga

Qy	486 cgttcaagtta
Dd	129 cggcagtaga

RESULT 10

```

US-09-388-906A-15677/C
; Sequence 15677, Application US/09388906A
; GENERAL INFORMATION:
; APPLICANT: Havukkala, Ilkka
; APPLICANT: Shenk, Michael Andrew
; TITLE OF INVENTION: Polynucleotides Isolated From Plants and
; TITLE OF INVENTION: Methods For Their Use
; FILE REFERENCE: 11000.1013U
; CURRENT APPLICATION NUMBER: US/09/388,906A
; CURRENT FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 24843
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15677
; LENGTH: 261
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(261)
; OTHER INFORMATION: n = A,T,C or G
; US-09-388-906A-15677

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	Query Match	2.18;	Score 33;	DB 5;	Length 261;
	Best Local Similarity	55.8%;	Pred. NO. 7.4;		
	Matches 63;	Conservative	0;	Mismatches 50;	Indels 0;
				Gaps	0;
QY	1178	ctgagtcctgcgcaatcccaaccgaagaaattctagtcgccatgccacaattgctga	1237		
Db	244	CGGAATTCCTCCCAAGAAATCGTCGCCAGTGGGTGCAGCGCTGCAGACACTGCAACTGCTGC	185		
QY	1238	gccttaagaacatgcctacgagctgccatgactcttgatctggtgcacaac	1290		
Db	184	GCCTTTAGAACCTTGAAGACGGCGCTGTCATCGATGATGCCCGGACACCCCTTC	132		

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RESULT 11
US-09-680-959-564
; Sequence 564, Application US/09680959
; GENERAL INFORMATION:
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Mutated Mammalian Cells and
; TITLE OF INVENTION: Animals
; FILE REFERENCE: LEX-0051-USA
; CURRENT APPLICATION NUMBER: US/09/680,959
; CURRENT FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/157,651
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 574
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 564
; LENGTH: 327
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-680-959-564

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[illegible]

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US-09-976-594-985/c
; Sequence 885, Application US/09976594
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program

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Query Match      2.1%; Score 32.4; DB 5; Length 14800;
Best Local Similarity 46.5%; Pred. No. 68;
Matches 105; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

QY 906 gcgggagtcacccaaagacgaacccagctcaatagcaagaagcgcaagtcctgcgcgga 965
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5883 gagcagcgccgaggtggaggaagatcctggcgtgaaggcgagcttcgagaaggc 5942
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 966 agccgcgaagaagatgagccgctccaaggtgcgtgcgtgcatgtataaagacggagga 1025
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5943 ggcgcgtggaagcgagagctggagctggagctggagctggagcga 6002
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1026 cagcgagagcaatagatagccgctccagactcgacgactccgcgcg 1085
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6003 cagctgcgacgaagcgagcgccgagctggagcgccgagcgagcgagctggcgcgcg 6062
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1086 gacacggatggcgattaccgtctggtatttaagtgccccaataag 1131
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6063 ggaggaggagcgcgccgctggagctggagagcgctgcagaag 6108
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15
US-09-834-975-451/C
; Sequence 451, Application US/09834975
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Brown, Jeffrey
; APPLICANT: Bolt, Andrew
; APPLICANT: Van Huffel, Christophe
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
; TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; FILE REFERENCE: MRI-016B
; CURRENT APPLICATION NUMBER: US/09/834, 975
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/197,538
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 1046
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 451
; LENGTH: 425
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(425)
; OTHER INFORMATION: n = A,T,C or G
US-09-834-975-451
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Query Match      2.0%; Score 32.2; DB 5; Length 425;
Best Local Similarity 52.3%; Pred. No. 15;
Matches 67; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 1429 aaagaacacattttatattttatagatatactgtgttaactgcagcttctatgtgac 1488
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 188 AAAAAAAAAACCCCTTTTTTTTTTTTGGGGAAATTTTTT 129
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1489 tacgtactttgtctacacacacatactctgtacacaaagccaaagtgatatt 1548
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 128 AATTTTTTTTTTTTTNNNNAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 69
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1549 attaaaga 1556
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 68 AAAAAAAA 61
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Search completed: November 16, 2001, 15:48:45
Job time: 5012 sec

Qy	121	AFNVDFVQFSKMPIQPLMLRVFLCFSDNDVSAPYVRCONHLSVEPLTANNAMKRESLLRSE	180
Db	121	AFNVDFVQFSKMPIQLPLMLRVFLCFSDNDVSAPYVRCONHLSVEPLTANNAMKRESLLRSE	180
Qy	181	NPNSVYCGNAQCKGTSERFSVVYPPLNMSRSVTRSGLTROT'LAFKFVQNSCIGRKETSIV	240
Db	181	NPNSVYCGNAQCKGTSERFSVVYPPLNMSRSVTRSGLTROT'LA-KFVQNSCIGRKETSIV	240
Qy	241	FCLBKACGDITVGQHVHWIKICTCPKRDRIODBRQLNSKKKSVPPEAAEDEDPSKVRCITA	300
Db	241	FCLBKACGDITVGQHVHWIKICTCPKRDRIQDBRQLNSKKKSVPPEAAEDEDPSKVRCITA	300
Qy	301	IKTETDESNDSCDDSAENWYSRTPDGQYRLAITCPKNEWLLOSIEGMKLEAAAEEVL	360
Db	301	IKTETDESNDSCDDSAENWYSRTPDGQYRLAITCPKNEWLLOSIEGMKLEAAAEEVL	360
Qy	361	NPNOENLRHHAKLLSLKKRAYELP	385
Db	361	NPNOENLRHHAKLLSLKKRAYELP	385

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RESULT      2
PCT-US00-06602A-2
? Sequence 2, Application PC/TUS00006602A
? GENERAL INFORMATION:
? APPLICANT: EXELIXIS, INC
? TITLE OF INVENTION: Insect p53 Tumor Suppressor Genes and Proteins
? FILE REFERENCE: Insect p53 sequences
? CURRENT APPLICATION NUMBER: PCT/US00/06602A
? CURRENT FILING DATE: 2000-03-13
? PRIOR APPLICATION NUMBER: EX99-001
? PRIOR FILING DATE: 1999-03-16
? NUMBER OF SEQ ID NOS: 22
? SOFTWARE: PatentIn ver. 2.1
? SEQ ID NO 2
? LENGTH: 385
? TYPE: PRT
? ORGANISM: Drosophila melanogaster
PCT-US00-06602A-2

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Query Match	100.0%	Score 2008;	DB 1;	Length 385;
Best Local Similarity	100.0%;	Pred. No. 7.4e-192;		
Matches 385;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps
Qy	1	MYISOPNSWKESTDESDSTDEV	IKEDIPKTVESGSELTPPMFLQGLNSGLNMQFS	60
Db	1	MYISOPNSWKESTDESDSTDEV	IKEDIPKTVESGSELTPPMFLQGLNSGLNMQFS	60
Qy	61	QQSVLRMMQLDIOIQANTPLK	ENHNIGYCFYSVMVLDEPPKSLWMYSTIPLNKLYIRMNK	120
Db	61	QQSVLRMMQLDIOIQANTPLK	ENHNIGYCFYSVMVLDEPPKSLWMYSTIPLNKLYIRMNK	120
Qy	121	AFNVDDQFKSMPTQPLNLRV	FLCFSDNVSAAPVRCQNHLSVEPLTANNAKMRESLSLSE	180
Db	121	AFNVDDQFKSMPTQPLNLRV	FLCFSDNVSAAPVRCQNHLSVEPLTANNAKMRESLSLSE	180
Qy	181	NFNSVYCGNAQGGISERE	SVVYPLNNKRSVTRSGITQTQTLAEKFVCQNSCIGRKETS	240
Db	181	NFNSVYCGNAQGGISERE	SVVYPLNNKRSVTRSGITQTQTLAEKFVCQNSCIGRKETS	240
Qy	241	FCLEKACDVGQHVTHVKICTC	PKRDIODERQNLNKKRSVPPEAAEDEFPSKYRRCIA	300
Db	241	FCLEKACDVGQHVTHVKICTC	PKRDIODERQNLNKKRSVPPEAAEDEFPSKYRRCIA	300
Qy	301	IKTETDESNDSDCDDSAAE	WNVSPTPDGYRLAITCPNKKWLLQSTEGMIKEAAAEVLR	360
Db	301	IKTETDESNDSDCDDSAAE	WNVSPTPDGYRLAITCPNKKWLLQSTEGMIKEAAAEVLR	360
Qy	361	NPNQENLRRHANKLLSLK	RAYELP 385	
Db	361	NPNQENLRRHANKLLSLK	RAYELP 385	

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RESULT 3
US-09-268-969-2
; Sequence 2, Application US/09268969
; GENERAL INFORMATION:
; APPLICANT: Buchman, Andrew R.
; APPLICANT: Platt, Darren M.
; APPLICANT: Ollmann, Michael M.
; APPLICANT: Young, Lynn M.
; APPLICANT: Demsky, Madelyn R.
; APPLICANT: Keesan, Kevin P.
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF D. MELANOGASTER TUMOR
; FILE REFERENCE: 7326-084
; CURRENT APPLICATION NUMBER: US/09/268.969
; CURRENT FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-268-969-2

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Query Match	100.0%;	Score 2008;	DB 16;	Length 385;
Best Local Similarity	100.0%;	Pred. No. 7.4e-192;		
Matches 385;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MYISQPSWKHSTSDSDSTVEDIKPKTVEYSGSELTTEPMFLOGINSGLMQFS	60	
Db	1	MYISQPSWKHSTSDSDSTVEDIKPKTVEYSGSELTTEPMFLOGINSGLMQFS	60	
Qy	61	QQSVLRREMLQDTIQOANTLPKLENNHINIGGYCFSMVLDEPPKSLMWYSIPLNKLYIRMK	120	
Db	61	QQSVLRREMLQDTIQOANTLPKLENNHINIGGYCFSMVLDEPPKSLMWYSIPLNKLYIRMK	120	
Qy	121	AFNVDVQFKSKMPIQPLNIRVFLCFSDNDYSAVPVQCQNHLSVEPLTANNKMRSELLRSE	180	
Db	121	AFNVDVQFKSKMPIQPLNIRVFLCFSDNDYSAVPVQCQNHLSVEPLTANNKMRSELLRSE	180	
Qy	181	NPNYSVYCGNAGKGISERFSVWVPLNMSRSVTRSGLTROTTLAFKVCQNSCTIGRKETSIV	240	
Db	181	NPNYSVYCGNAGKGISERFSVWVPLNMSRSVTRSGLTROTTLAFKVCQNSCTIGRKETSIV	240	
Qy	241	FCLEKACGDIVGQHVTHVKICTCPKRDRIQDERQLNSKKRKSYPEAAEDPEFSKVRRCIA	300	
Db	241	FCLEKACGDIVGQHVTHVKICTCPKRDRIQDERQLNSKKRKSYPEAAEDPEFSKVRRCIA	300	
Qy	301	IKTETETNSRCDSDSAEENNVSRTPDGDYRLATITCPNKEWLLQSTIGMTKEAAAAEVLR	360	
Db	301	IKTETETNSRCDSDSAEENNVSRTPDGDYRLATITCPNKEWLLQSTIGMTKEAAAAEVLR	360	
Qy	361	NPNQENLRHANKILLSKKRAYELP	385	
Db	361	NPNQENLRHANKILLSKKRAYELP	385	

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RESULT      4
US-09-524-101-2
; Sequence 2, Application US/09524101
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: Insect p53 Tumor Suppressor Genes and Proteins
; FILE REFERENCE: Insect p53 EX00-015
; CURRENT APPLICATION NUMBER: US/09/524, 101
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 09/268, 969
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/184, 373
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.0

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```
; SEQ ID NO 2
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-524-101-2

Query Match      100.0%; Score 2008; DB 19; Length 385;
Best Local Similarity 100.0%; Pred. No. 7.4e-192;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYISQPMWHKSTEDSDTEVDIKEDIPKTVESGSELTTEPMAFLQGLNSGMLMQFS 60
DB 1 MYISQPMWHKSTEDSDTEVDIKEDIPKTVESGSELTTEPMAFLQGLNSGMLMQFS 60

QY 61 QOSVLRMMQLDIOIQANTLPKLENNHIGGCFSMVLDEPPKSLWMSYIPLNKLIRMNK 120
DB 61 QOSVLRMMQLDIOIQANTLPKLENNHIGGCFSMVLDEPPKSLWMSYIPLNKLIRMNK 120

QY 121 AFNVDVQFKSKMPTQPLNLRVFLCFSDNDVSAPVVRQCNHLSVEPLTANNAKRESLLRSE 180
DB 121 AFNVDVQFKSKMPTQPLNLRVFLCFSDNDVSAPVVRQCNHLSVEPLTANNAKRESLLRSE 180

QY 181 NPNSVYCGNAQKGISERFSVVPVPLNMSRVSRTSGLTROTFLAFKFCVQNSCIGRKETSIV 240
DB 181 NPNSVYCGNAQKGISERFSVVPVPLNMSRVSRTSGLTROTFLAFKFCVQNSCIGRKETSIV 240

QY 241 FCLEKACGDIVGQHVHVICTCPKRDRIQDERQLNSKKRKSVPAAAEDEPSKVRRCIA 300
DB 241 FCLEKACGDIVGQHVHVICTCPKRDRIQDERQLNSKKRKSVPAAAEDEPSKVRRCIA 300

QY 301 IKTEDESNDSDCDDSAAEWNVSRTPDGYRLAITCPNKEWLLQSGIEGMIKEAAAEVLR 360
DB 301 IKTEDESNDSDCDDSAAEWNVSRTPDGYRLAITCPNKEWLLQSGIEGMIKEAAAEVLR 360

QY 361 NPQENLRHANKLLSLKKR 380
DB 361 NPQENLRHANKLLSLKKR 380

Query Match      98.3%; Score 1973; DB 24; Length 381;
Best Local Similarity 99.5%; Pred. No. 2.4e-188;
Matches 378; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MYISQPMWHKSTEDSDTEVDIKEDIPKTVESGSELTTEPMAFLQGLNSGMLMQFS 60
DB 1 MYISQPMWHKSTEDSDTEVDIKEDIPKTVESGSELTTEPMAFLQGLNSGMLMQFS 60

QY 61 QOSVLRMMQLDIOIQANTLPKLENNHIGGCFSMVLDEPPKSLWMSYIPLNKLIRMNK 120
DB 61 QOSVLRMMQLDIOIQANTLPKLENNHIGGCFSMVLDEPPKSLWMSYIPLNKLIRMNK 120

QY 121 AFNVDVQFKSKMPTQPLNLRVFLCFSDNDVSAPVVRQCNHLSVEPLTANNAKRESLLRSE 180
DB 121 AFNVDVQFKSKMPTQPLNLRVFLCFSDNDVSAPVVRQCNHLSVEPLTANNAKRESLLRSE 180

QY 181 NPNSVYCGNAQKGISERFSVVPVPLNMSRVSRTSGLTROTFLAFKFCVQNSCIGRKETSIV 240
DB 181 NPNSVYCGNAQKGISERFSVVPVPLNMSRVSRTSGLTROTFLAFKFCVQNSCIGRKETSIV 240

QY 241 FCLEKACGDIVGQHVHVICTCPKRDRIQDERQLNSKKRKSVPAAAEDEPSKVRRCIA 300
DB 241 FCLEKACGDIVGQHVHVICTCPKRDRIQDERQLNSKKRKSVPAAAEDEPSKVRRCIA 300

QY 301 IKTEDESNDSDCDDSAAEWNVSRTPDGYRLAITCPNKEWLLQSGIEGMIKEAAAEVLR 360
DB 301 IKTEDESNDSDCDDSAAEWNVSRTPDGYRLAITCPNKEWLLQSGIEGMIKEAAAEVLR 360

QY 361 NPQENLRHANKLLSLKKR 380
DB 361 NPQENLRHANKLLSLKKR 380

Query Match      98.3%; Score 1973; DB 24; Length 381;
Best Local Similarity 99.5%; Pred. No. 2.4e-188;
Matches 378; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MYISQPMWHKSTEDSDTEVDIKEDIPKTVESGSELTTEPMAFLQGLNSGMLMQFS 60
DB 1 MYISQPMWHKSTEDSDTEVDIKEDIPKTVESGSELTTEPMAFLQGLNSGMLMQFS 60

QY 61 QOSVLRMMQLDIOIQANTLPKLENNHIGGCFSMVLDEPPKSLWMSYIPLNKLIRMNK 120
DB 61 QOSVLRMMQLDIOIQANTLPKLENNHIGGCFSMVLDEPPKSLWMSYIPLNKLIRMNK 120

QY 121 AFNVDVQFKSKMPTQPLNLRVFLCFSDNDVSAPVVRQCNHLSVEPLTANNAKRESLLRSE 180
DB 121 AFNVDVQFKSKMPTQPLNLRVFLCFSDNDVSAPVVRQCNHLSVEPLTANNAKRESLLRSE 180

QY 181 NPNSVYCGNAQKGISERFSVVPVPLNMSRVSRTSGLTROTFLAFKFCVQNSCIGRKETSIV 240
DB 181 NPNSVYCGNAQKGISERFSVVPVPLNMSRVSRTSGLTROTFLAFKFCVQNSCIGRKETSIV 240

QY 241 FCLEKACGDIVGQHVHVICTCPKRDRIQDERQLNSKKRKSVPAAAEDEPSKVRRCIA 300
DB 241 FCLEKACGDIVGQHVHVICTCPKRDRIQDERQLNSKKRKSVPAAAEDEPSKVRRCIA 300

QY 301 IKTEDESNDSDCDDSAAEWNVSRTPDGYRLAITCPNKEWLLQSGIEGMIKEAAAEVLR 360
DB 301 IKTEDESNDSDCDDSAAEWNVSRTPDGYRLAITCPNKEWLLQSGIEGMIKEAAAEVLR 360

QY 361 NPQENLRHANKLLSLKKR 380
DB 361 NPQENLRHANKLLSLKKR 380

Query Match      98.3%; Score 1973; DB 24; Length 381;
Best Local Similarity 99.5%; Pred. No. 2.4e-188;
Matches 378; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MYISQPMWHKSTEDSDTEVDIKEDIPKTVESGSELTTEPMAFLQGLNSGMLMQFS 60
DB 1 MYISQPMWHKSTEDSDTEVDIKEDIPKTVESGSELTTEPMAFLQGLNSGMLMQFS 60

QY 61 QOSVLRMMQLDIOIQANTLPKLENNHIGGCFSMVLDEPPKSLWMSYIPLNKLIRMNK 120
DB 61 QOSVLRMMQLDIOIQANTLPKLENNHIGGCFSMVLDEPPKSLWMSYIPLNKLIRMNK 120

QY 121 AFNVDVQFKSKMPTQPLNLRVFLCFSDNDVSAPVVRQCNHLSVEPLTANNAKRESLLRSE 180
DB 121 AFNVDVQFKSKMPTQPLNLRVFLCFSDNDVSAPVVRQCNHLSVEPLTANNAKRESLLRSE 180
```

```
RESULT 6
US-60-171-625-450
; Sequence 450, Application US/60171625
; GENERAL INFORMATION:
; APPLICANT: Skupski, Marian
; TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS THAT SHOW
; TITLE OF INVENTION: HIGH HOMOLOGY TO KNOWN HUMAN DISEASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000179
; CURRENT APPLICATION NUMBER: US/60/171,625
; CURRENT FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 450
; LENGTH: 381
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-60-171-625-450

Query Match      98.3%; Score 1973; DB 24; Length 381;
Best Local Similarity 99.5%; Pred. No. 2.4e-188;
Matches 378; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MYISQPMWHKSTEDSDTEVDIKEDIPKTVESGSELTTEPMAFLQGLNSGMLMQFS 60
DB 1 MYISQPMWHKSTEDSDTEVDIKEDIPKTVESGSELTTEPMAFLQGLNSGMLMQFS 60

QY 61 QOSVLRMMQLDIOIQANTLPKLENNHIGGCFSMVLDEPPKSLWMSYIPLNKLIRMNK 120
DB 61 QOSVLRMMQLDIOIQANTLPKLENNHIGGCFSMVLDEPPKSLWMSYIPLNKLIRMNK 120

QY 121 AFNVDVQFKSKMPTQPLNLRVFLCFSDNDVSAPVVRQCNHLSVEPLTANNAKRESLLRSE 180
DB 121 AFNVDVQFKSKMPTQPLNLRVFLCFSDNDVSAPVVRQCNHLSVEPLTANNAKRESLLRSE 180

QY 181 NPNSVYCGNAQKGISERFSVVPVPLNMSRVSRTSGLTROTFLAFKFCVQNSCIGRKETSIV 240
DB 181 NPNSVYCGNAQKGISERFSVVPVPLNMSRVSRTSGLTROTFLAFKFCVQNSCIGRKETSIV 240

QY 241 FCLEKACGDIVGQHVHVICTCPKRDRIQDERQLNSKKRKSVPAAAEDEPSKVRRCIA 300
DB 241 FCLEKACGDIVGQHVHVICTCPKRDRIQDERQLNSKKRKSVPAAAEDEPSKVRRCIA 300

QY 301 IKTEDESNDSDCDDSAAEWNVSRTPDGYRLAITCPNKEWLLQSGIEGMIKEAAAEVLR 360
DB 301 IKTEDESNDSDCDDSAAEWNVSRTPDGYRLAITCPNKEWLLQSGIEGMIKEAAAEVLR 360

QY 361 NPQENLRHANKLLSLKKR 380
DB 361 NPQENLRHANKLLSLKKR 380
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Db 17 LAEWGDNMDNLNFEKDEPTLNDNLNYNLIANGSIVANDSKVHLIFPGVOTVSPNDXY 76
QY 87 NIGGYCFSVLDEPP---KSLWYMSIPLNKLYIRMKAFNVDOFKSKMPTQPLNLRVEL 143
Db 77 D-GPYE--VDVHTVAKNSWVSTTLNKVYTMGSPFPVDFRY-SHRPNPLFIR--- 129
QY 144 CFSNDV-SAP-----VVRCONHLSVEPLTANNAK--MRESLLRSENPNNSVYCGNAQKG 194
Db 130 --STPYVSAPOAEQCVRYCLNHEFSKESDGLKEHPIHRCANQYAYALGD---KS 184
QY 195 ISERFSVPLNMSRVTRSGLTROTAFKVCQNSC-----IGRKETSLVFCLEKACGDI 250
Db 185 KNERLSVPIFGIPQTGES--VRE--IFEVCKNSCPGMMNRRAVEIIFTLEDNOGTII 240
QY 251 VGOHVHVKTCTCPKRDRIODE-----ROLNSKKRSVPEAAEEDPSKVR 296
Db 241 YGRKTLNVRICSPKRDKEKDEKONTANTNLPHGKRRKMEKPSKAPMOTQEND-TKEFT 299
QY 297 RCIAKTEDTESNDSRDDCSAAE---WNYSRTPDGDYRLAITCPNKWLLQSTEGMIKE 353
Db 300 LTIPLVGRHNEQVLYKCHDLWAGELRNIGNGTEGPKYIA-----LNKINTLIRE 350
QY 354 AA 355
Db 351 SS 352

RESULT 13
PCT-US00-06602-6
; Sequence 6, Application PC/TUS00006602
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC
; TITLE OF INVENTION: Insect p53 Tumor Suppressor Genes and Proteins
; FILE REFERENCE: Insect p53 sequences
; CURRENT APPLICATION NUMBER: PCT/US00/06602
; EARLIER FILING DATE: 2000-03-15
; EARLIER FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Tribolium castaneum
PCT-US00-06602-6

Query Match 12.3%; Score 247.5; DB 1, Length 350;
Best Local Similarity 24.2%; Pred. No. 2.3e-15;
Matches 88; Conservative 67; Mismatches 124; Indels 85; Gaps 17;

QY 25 IKEDIPKTVESGSELTTEPMAFLQGLNSGLMFOFSQSVLRMMML---QDIQIQANTLP 81
Db 23 LKDDVGRIMHNNVHLND-----DGEEEKYSNEANYTESIFPPDQPTNLGTEYP 73
QY 82 KLENHNIIGGYCFSWLD-BPPKSLWMSIPLNKLYIRMKAFNVDOFKSKMPTQPLNLR 140
Db 74 -----GPNFNSVLISPNQKSPNEYSEKLNKIFIGINVKFPVAFSVQNRPNPLVIR 126
QY 141 VFLCFS-----NDVSAPVYRCQNHLSVEPLTANNAKMR---ESLLRSENPNNSVYCGNAQ 191
Db 127 ATPVFSQTQHFQDL---VHRCVGRH--HPQDSNKGAVAPHIFQHIIRCTNDNALYFGD-- 179
QY 192 GKGISERFSVVVPL---NMSRSVTRSGLTROTAFKVCQNSC---IGRKETSLVFCLEK 245
Db 180 -KNTGTRNLNIVLPLAHPOGVEDVWKE-----FFQVCKNSCPLGMNRRPIDVFTLED 231
QY 246 ACGDIVGQHVHVKTCTCPKRDRIODEROLNSKKRSVPEAAEEDPSKVRRCIAIKTED 305
Db 232 NKGVEFGRRLVGVRCVSCPKRDKKEKDMES-----AVP-----PRKKRKL----- 274
QY 306 TESNDSRDCDDSAEAWNVSRTPDG-----YRLAITCPNKWLLQSTEGMIKEAAAEVLR 360

Db 275 --GNDERRV-----VPGSSDNKIFALNIHIPGKKNYLAQKMCQDMLANEILK 321
QY 361 NPNQ 364
Db 322 KQEQ 325
RESULT 14
PCT-US00-06602A-6
; Sequence 6, Application PC/TUS00006602A
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC
; TITLE OF INVENTION: Insect p53 Tumor Suppressor Genes and Proteins
; FILE REFERENCE: Insect p53 sequences
; CURRENT APPLICATION NUMBER: PCT/US00/06602A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: EX99-001
; PRIOR FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Tribolium castaneum
PCT-US00-06602A-6

Query Match 12.3%; Score 247.5; DB 1; Length 350;
Best Local Similarity 24.2%; Pred. No. 2.3e-15;
Matches 88; Conservative 67; Mismatches 124; Indels 85; Gaps 17;

QY 25 IKEDIPKTVESGSELTTEPMAFLQGLNSGLMFOFSQSVLRMMML---QDIQIQANTLP 81
Db 23 LKDDVGRIMHNNVHLND-----DGEEEKYSNEANYTESIFPPDQPTNLGTEYP 73
QY 82 KLENHNIIGGYCFSWLD-BPPKSLWMSIPLNKLYIRMKAFNVDOFKSKMPTQPLNLR 140
Db 74 -----GPNFNSVLISPNQKSPNEYSEKLNKIFIGINVKFPVAFSVQNRPNPLVIR 126
QY 141 VFLCFS-----NDVSAPVYRCQNHLSVEPLTANNAKMR---ESLLRSENPNNSVYCGNAQ 191
Db 127 ATPVFSQTQHFQDL---VHRCVGRH--HPQDSNKGAVAPHIFQHIIRCTNDNALYFGD-- 179
QY 192 GKGISERFSVVVPL---NMSRSVTRSGLTROTAFKVCQNSC---IGRKETSLVFCLEK 245
Db 180 -KNTGTRNLNIVLPLAHPOGVEDVWKE-----FFQVCKNSCPLGMNRRPIDVFTLED 231
QY 246 ACGDIVGQHVHVKTCTCPKRDRIODEROLNSKKRSVPEAAEEDPSKVRRCIAIKTED 305
Db 232 NKGVEFGRRLVGVRCVSCPKRDKKEKDMES-----AVP-----PRKKRKL----- 274
QY 306 TESNDSRDCDDSAEAWNVSRTPDG-----YRLAITCPNKWLLQSTEGMIKEAAAEVLR 360
Db 275 --GNDERRV-----VPGSSDNKIFALNIHIPGKKNYLAQKMCQDMLANEILK 321
QY 361 NPNQ 364
Db 322 KQEQ 325

RESULT 15
US-09-524-101-6
; Sequence 6, Application US/09524101
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: Insect p53 Tumor Suppressor Genes and Proteins
; FILE REFERENCE: Insect p53 EX00-015
; CURRENT APPLICATION NUMBER: US/09/524,101
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 09/268,969
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/184,373

; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent version 3.0
; SEQ ID NO 6
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Tribolium castaneum
US-09-524-101-6

Query Match 12.3%; Score 247.5; DB 19; Length 350;
Best Local Similarity 24.2%; Pred. No. 2.3e-15;
Matches 88; Conservative 67; Mismatches 124; Indels 85; Gaps 17;

QY	25	IKEDIPKTVESGSELTTEPMAFLQGLNSGLMFOFSQSVLREMLL---	QDIQIQAANTLP	81
DB	23	LKDDVGRIHNNVHLVND-----DGEKEYSNEANYTESIFPDQPTNLGTTEYP		73
QY	82	KLENHNIGGYCFSMVLID-EPPKSLMYSIPLNKLYIRMNKAFNVDPQKSKMPTQPLNLR		140
DB	74	-----GPFNSVLISPNQKSPWEYSEKLNKIFIGINVKFPVAFSVQNRPNPLPIR		126
QY	141	VFLCFS-----NDVSAPVVRCONHLSVEPLTANNAMR-----ESLLRSENPNSVCGNAQ		191
DB	127	ATPVFSQTHFQDL---VHRCVGRH--HPQDSNKGVAHFHFQIIRCTNDNALYFGD--		179
QY	192	CGKISERFSVVVPL---NMSRSVTSRSLTROTALAFKVCQNSC---IGRKETSLVFCLEK		245
DB	180	-KNTGTRLNIVLPLAHPQGVGVKE-----FFQVCKNSCPLGMNRRPIDVVFTELED		231
QY	246	ACGDIVGQHVHVKICTPKDRIDQERQLNSKKRSVPEAAEEDPESKVRRCIAIKTED		305
DB	232	NKGEVFGRLVGVVVCSPKRDKEEDMES-----AVP-----PRKKRKL-----		274
QY	306	TESNDSRDCDDSAEAWNVSRTPDGD-----YRLAITCPNKENLLOSIEGMIKEAAAEVLR		360
DB	275	--GNDERRV-----VPQGSNDKLEA--NIHIPGKNYLOALKMCDMLANEILK		321
QY	361	NPNQ	364	
DB	322	KOEQ	325	

Search completed: November 16, 2001, 15:55:05
Job time: 472 sec


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RESULT 2
US-09-850-716A-344
; Sequence 344, Application US/09850716A
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-344

Query Match          9.3%; Score 186; DB 5; Length 516;
Best Local Similarity 22.2%; Pred. No. 3.1e-10;
Matches 75; Conservative 59; Mismatches 124; Indels 80; Gaps 15;

QY 5 QPMSWHKSTDESDST-EVDIKEDIPKTVESGSELTTEPMAFLQGLNSGMLMFOFSQOS 63
Db 31 QPIDLNFVDEPSEDGATNKIEISMD---CIRMQSDSL-SDPM-----WPQYTNLG 76
QY 64 VIREMMLQDIQI---ANTLPKLENH-----NI 88
Db 77 LLNSM---DQIQNGSSSTPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAINSTDYP 133
QY 89 GGYCFSMVLDE---PPKSLMWYSIPLNKLYIRMKAFNVDQFKSKMPTQPLNLRVLCF 145
Db 134 GPHSFDVSFOQSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPP-QGAVIRAMPVY 192
QY 146 --SNDVSAPVVRCONHLSVEPLTANNAKMRSLRSENPNVSYCGNAQKGISE-----RF 199
Db 193 KKAHVTEVVKRCPNHLSREFNEQIAPPSHLIRVE-----GNSHAQYVEDPITGRQ 245
QY 200 SVVYPLNMSRSVTRSGLTQTTLAFKVFQNSCIG---RKETSIVFCLEKACGDIVGQHV 256
Db 246 SVLVYP---EPPQVGTEFTTLYNFMCSNCSVGMNRRPILIIVTLETRODQVILGRRCF 301
QY 257 HVKICTCPKRDRIQDERQLNSKKRKSVPPEAAEEDPSK 294
Db 302 ERICACPGRRKRADE---DSIRKQOVSDSKNGDGTK 336

RESULT 3
US-09-850-716A-339
; Sequence 339, Application US/09850716A
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-339

Query Match          9.3%; Score 186; DB 5; Length 641;
Best Local Similarity 22.2%; Pred. No. 4.2e-10;
Matches 75; Conservative 59; Mismatches 124; Indels 80; Gaps 15;

QY 5 QPMSWHKSTDESDST-EVDIKEDIPKTVESGSELTTEPMAFLQGLNSGMLMFOFSQOS 63
Db 31 QPIDLNFVDEPSEDGATNKIEISMD---CIRMQSDSL-SDPM-----WPQYTNLG 76
QY 64 VIREMMLQDIQI---ANTLPKLENH-----NI 88
Db 77 LLNSM---DQIQNGSSSTPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAINSTDYP 133
QY 89 GGYCFSMVLDE---PPKSLMWYSIPLNKLYIRMKAFNVDQFKSKMPTQPLNLRVLCF 145
Db 134 GPHSFDVSFOQSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPP-QGAVIRAMPVY 192
QY 146 --SNDVSAPVVRCONHLSVEPLTANNAKMRSLRSENPNVSYCGNAQKGISE-----RF 199
Db 193 KKAHVTEVVKRCPNHLSREFNEQIAPPSHLIRVE-----GNSHAQYVEDPITGRQ 245
QY 200 SVVYPLNMSRSVTRSGLTQTTLAFKVFQNSCIG---RKETSIVFCLEKACGDIVGQHV 256
Db 246 SVLVYP---EPPQVGTEFTTLYNFMCSNCSVGMNRRPILIIVTLETRODQVILGRRCF 301
QY 257 HVKICTCPKRDRIQDERQLNSKKRKSVPPEAAEEDPSK 294
Db 302 ERICACPGRRKRADE---DSIRKQOVSDSKNGDGTK 336

Query Match          9.3%; Score 186; DB 5; Length 680;
Best Local Similarity 22.2%; Pred. No. 4.6e-10;
Matches 75; Conservative 59; Mismatches 124; Indels 80; Gaps 15;

QY 5 QPMSWHKSTDESDST-EVDIKEDIPKTVESGSELTTEPMAFLQGLNSGMLMFOFSQOS 63
Db 70 QPIDLNFVDEPSEDGATNKIEISMD---CIRMQSDSL-SDPM-----WPQYTNLG 115
QY 64 VIREMMLQDIQI---ANTLPKLENH-----NI 88
Db 116 LLNSM---DQIQNGSSSTPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAINSTDYP 172
QY 89 GGYCFSMVLDE---PPKSLMWYSIPLNKLYIRMKAFNVDQFKSKMPTQPLNLRVLCF 145
Db 173 GPHSFDVSFOQSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPP-QGAVIRAMPVY 231
QY 146 --SNDVSAPVVRCONHLSVEPLTANNAKMRSLRSENPNVSYCGNAQKGISE-----RF 199
Db 232 KKAHVTEVVKRCPNHLSREFNEQIAPPSHLIRVE-----GNSHAQYVEDPITGRQ 284
QY 200 SVVYPLNMSRSVTRSGLTQTTLAFKVFQNSCIG---RKETSIVFCLEKACGDIVGQHV 256
Db 285 SVLVYP---EPPQVGTEFTTLYNFMCSNCSVGMNRRPILIIVTLETRODQVILGRRCF 340
QY 257 HVKICTCPKRDRIQDERQLNSKKRKSVPPEAAEEDPSK 294
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Matches 75; Conservative 59; Mismatches 124; Indels 80; Gaps 15;

QY 5 QPMSWHKSTDESDST-EVDIKEDIPKTVESGSELTTEPMAFLQGLNSGMLMFOFSQOS 63
Db 31 QPIDLNFVDEPSEDGATNKIEISMD---CIRMQSDSL-SDPM-----WPQYTNLG 76
QY 64 VIREMMLQDIQI---ANTLPKLENH-----NI 88
Db 77 LLNSM---DQIQNGSSSTPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAINSTDYP 133
QY 89 GGYCFSMVLDE---PPKSLMWYSIPLNKLYIRMKAFNVDQFKSKMPTQPLNLRVLCF 145
Db 134 GPHSFDVSFOQSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPP-QGAVIRAMPVY 192
QY 146 --SNDVSAPVVRCONHLSVEPLTANNAKMRSLRSENPNVSYCGNAQKGISE-----RF 199
Db 193 KKAHVTEVVKRCPNHLSREFNEQIAPPSHLIRVE-----GNSHAQYVEDPITGRQ 245
QY 200 SVVYPLNMSRSVTRSGLTQTTLAFKVFQNSCIG---RKETSIVFCLEKACGDIVGQHV 256
Db 246 SVLVYP---EPPQVGTEFTTLYNFMCSNCSVGMNRRPILIIVTLETRODQVILGRRCF 301
QY 257 HVKICTCPKRDRIQDERQLNSKKRKSVPPEAAEEDPSK 294
Db 302 ERICACPGRRKRADE---DSIRKQOVSDSKNGDGTK 336

RESULT 4
US-09-850-716A-342
; Sequence 342, Application US/09850716A
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 680
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-342

Query Match          9.3%; Score 186; DB 5; Length 680;
Best Local Similarity 22.2%; Pred. No. 4.6e-10;
Matches 75; Conservative 59; Mismatches 124; Indels 80; Gaps 15;

QY 5 QPMSWHKSTDESDST-EVDIKEDIPKTVESGSELTTEPMAFLQGLNSGMLMFOFSQOS 63
Db 70 QPIDLNFVDEPSEDGATNKIEISMD---CIRMQSDSL-SDPM-----WPQYTNLG 115
QY 64 VIREMMLQDIQI---ANTLPKLENH-----NI 88
Db 116 LLNSM---DQIQNGSSSTPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAINSTDYP 172
QY 89 GGYCFSMVLDE---PPKSLMWYSIPLNKLYIRMKAFNVDQFKSKMPTQPLNLRVLCF 145
Db 173 GPHSFDVSFOQSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPP-QGAVIRAMPVY 231
QY 146 --SNDVSAPVVRCONHLSVEPLTANNAKMRSLRSENPNVSYCGNAQKGISE-----RF 199
Db 232 KKAHVTEVVKRCPNHLSREFNEQIAPPSHLIRVE-----GNSHAQYVEDPITGRQ 284
QY 200 SVVYPLNMSRSVTRSGLTQTTLAFKVFQNSCIG---RKETSIVFCLEKACGDIVGQHV 256
Db 285 SVLVYP---EPPQVGTEFTTLYNFMCSNCSVGMNRRPILIIVTLETRODQVILGRRCF 340
QY 257 HVKICTCPKRDRIQDERQLNSKKRKSVPPEAAEEDPSK 294
```


; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-338

Query Match 8.9%; Score 178; DB 5; Length 586;

Best Local Similarity 25.6%; Pred. No. 2,le-09;

Matches 51; Conservative 38; Mismatches 86; Indels 24; Gaps

7;

QY 105 WMYSIPLNKLIRMKAFNVQVQFQSKMPIOPLNLRVFLCF- SNDSYAPVVRCONHLSV 162

DB 98 WTYSTELKKLYCQIAKTPQIQKWTPTPP-OGAVIRMPVYKAEHVTEVVKRCPNHLS 156

QY 163 EPLTANNAMKRESLLRSENPNVYCGNAQKGISE-----RFSVVVPLNMSSVTRSLTR 218

DB 157 REFNEGQIAPPSHLRVE-----GNSHAQYVEDPITGRQSVLPVY-----EPQVQGTGF 205

QY 219 QTLAFVFCVQNSCIG---RKETSLVFLCEKACDVGQHVHVKICTCPKRDRIQDERQL 275

DB 206 TTVLYNFMCSNCGVMNRPIIIVTLETRDQVGLGRRCFEARICACPGDRKADE--- 262

QY 276 NSKKRKSVPFAAEDEPSK 294

DB 263 DSIKQOVSDSTKNGDGTK 281

RESULT 9

US-09-609-360C-15

; Sequence 15, Application US/09609360C

; GENERAL INFORMATION:

; APPLICANT: Hodge, Martin R.

; APPLICANT: Meyers, Rachel

; APPLICANT: Williamson, Mark

; TITLE OF INVENTION: Novel Kinases and Uses Thereof

; FILE REFERENCE: MP11999-096CP2

; CURRENT APPLICATION NUMBER: US/09/609,360C

; CURRENT FILING DATE: 2000-06-30

; PRIOR FILING DATE: 2000-05-01

; PRIOR FILING DATE: 2000-05-01

; PRIOR FILING DATE: 1999-06-30

; NUMBER OF SEQ ID NOS: 83

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 15

; LENGTH: 645

; TYPE: PRT

; ORGANISM: Arabidopsis thaliana

US-09-609-360C-15

Query Match 4.9%; Score 98.5; DB 5; Length 645;

Best Local Similarity 19.0%; Pred. No. 0.074;

Matches 85; Conservative 57; Mismatches 155; Indels 151; Gaps 18;

QY 4 SQPMWSHKESTDSEDSTEDVTDIKEDIPKTVVSGSELTPMPAFLOGNSGMLQFSSQS 63

DB 40 TDCPNW-----EGVKCMKGRVSKLVLENLNLGSLNGSLNQLDQLR 82

QY 64 VLREMLQDIOIQANTLP-----KLENNHIGGYCFSWLDEPPKSLW--- 105

DB 83 VL-----SFKGNSLGSIPNLGLVNLKSLYLNNDNFSG-----EPESLTSLSH 126

QY 106 -----MYSIPLNKLIRMKAFNVQVQ---FKSKMPIOPLN---LRVFLCFSDV 149

DB 127 RLKTVVLSRNFPSCKIPSSLLRLSLRYFYVDNLFSGIP--PLNQATLRFNFVSNQOL 184

QY 150 SA--PVWRQNHLSVEPLTANNAMKRESLLRSENPNVYCGNAQKGISERFSVVVPLNM 207

DB 185 SGHIPPTQALNRFNSESFTDIALCGDQIONS-----CNDTGTITSPSAKPAIPVAK 237

QY 208 SRSVTRSLTRQTLAFVFCVQNSCIGRKETSLVFLCEKACDVGQHVHVKICTCPKRD 267

DB 238 TRSRTK-----LIGITSGSI-----CGGILLILLTFLLCILWRK 273

QY 106 -----MYSIPLNKLIRMKAFNVQVQ---FKSKMPIOPLN---LRVFLCFSDV 149

DB 127 RLKTVVLSRNFPSCKIPSSLLRLSLRYFYVDNLFSGIP--PLNQATLRFNFVSNQOL 184

QY 150 SA--PVWRQNHLSVEPLTANNAMKRESLLRSENPNVYCGNAQKGISERFSVVVPLNM 207

DB 185 SGHIPPTQALNRFNSESFTDIALCGDQIONS-----CNDTGTITSPSAKPAIPVAK 237

QY 208 SRSVTRSLTRQTLAFVFCVQNSCIGRKETSLVFLCEKACDVGQHVHVKICTCPKRD 267

DB 238 TRSRTK-----LIGITSGSI-----CGGILLILLTFLLCILWRK 273

QY 268 RIQDERQLNSKKRKSVPFAAEDEPSKVRRCIAIKTETEDTESNDSRCDSDSAEAVNVSKTP 327

DB 274 RSKSKRE--ERRSKRVAESKE-----AKTAETEGTS-DQKNKRFSNE-KESE 317

QY 328 DGDYRLAITCPNKKEWLLQSGEMIKKEAAAEVLNR----- 361

DB 318 EGSVGTILVFLGRDITVYRYTMDLLKASAEITLGRGLTGLSTYKAVMESGFIITVKRLKDAG 377

QY 362 -PNQENLRHRHANKLLSLKK-----RAY 382

DB 378 FPRMDEFKRRIEILGRKHPNLVPLRAY 405

RESULT 10

US-09-609-360C-16

; Sequence 16, Application US/09609360C

; GENERAL INFORMATION:

; APPLICANT: Hodge, Martin R.

; APPLICANT: Meyers, Rachel

; APPLICANT: Williamson, Mark

; TITLE OF INVENTION: Novel Kinases and Uses Thereof

; FILE REFERENCE: MP11999-096CP2

; CURRENT APPLICATION NUMBER: US/09/609,360C

; CURRENT FILING DATE: 2000-06-30

; PRIOR FILING DATE: 2000-05-01

; PRIOR FILING DATE: 2000-05-01

; PRIOR FILING DATE: 1999-06-30

; NUMBER OF SEQ ID NOS: 83

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 16

; LENGTH: 645

; TYPE: PRT

; ORGANISM: Arabidopsis thaliana

US-09-609-360C-16

Query Match 4.9%; Score 98.5; DB 5; Length 645;

Best Local Similarity 19.0%; Pred. No. 0.074;

Matches 85; Conservative 57; Mismatches 155; Indels 151; Gaps 18;

QY 4 SQPMWSHKESTDSEDSTEDVTDIKEDIPKTVVSGSELTPMPAFLOGNSGMLQFSSQS 63

DB 40 TDCPNW-----EGVKCMKGRVSKLVLENLNLGSLNGSLNQLDQLR 82

QY 64 VLREMLQDIOIQANTLP-----KLENNHIGGYCFSWLDEPPKSLW--- 105

DB 83 VL-----SFKGNSLGSIPNLGLVNLKSLYLNNDNFSG-----EPESLTSLSH 126

QY 106 -----MYSIPLNKLIRMKAFNVQVQ---FKSKMPIOPLN---LRVFLCFSDV 149

DB 127 RLKTVVLSRNFPSCKIPSSLLRLSLRYFYVDNLFSGIP--PLNQATLRFNFVSNQOL 184

QY 150 SA--PVWRQNHLSVEPLTANNAMKRESLLRSENPNVYCGNAQKGISERFSVVVPLNM 207

DB 185 SGHIPPTQALNRFNSESFTDIALCGDQIONS-----CNDTGTITSPSAKPAIPVAK 237

QY 208 SRSVTRSLTRQTLAFVFCVQNSCIGRKETSLVFLCEKACDVGQHVHVKICTCPKRD 267

DB 238 TRSRTK-----LIGITSGSI-----CGGILLILLTFLLCILWRK 273

QY 268 RIQDERQLNSKKRKSVPFAAEDEPSKVRRCIAIKTETEDTESNDSRCDSDSAEAVNVSKTP 327

DB 274 RSKSKRE--ERRSKRVAESKE-----AKTAETEGTS-DQKNKRFSNE-KESE 317

QY 328 DGDYRLAITCPNKKEWLLQSGEMIKKEAAAEVLNR----- 361

DB 318 EGSVGTILVFLGRDITVYRYTMDLLKASAEITLGRGLTGLSTYKAVMESGFIITVKRLKDAG 377

QY 362 -PNQENLRHRHANKLLSLKK-----RAY 382

DB 378 FPRMDEFKRRIEILGRKHPNLVPLRAY 405


```

RESULT 11
US-09-345-473E-15
; Sequence 15, Application US/09345473E
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin
; TITLE OF INVENTION: Novel Kinases and Uses thereof
; FILE REFERENCE: 35800/183781
; CURRENT APPLICATION NUMBER: US/09/345,473E
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 645
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-345-473E-15

```

Query Match	4.98;	Score	98.5;	DB	5;	Length	645;
Best Local Similarity	19.0%;	Pred.	No. 0.074;				
Matches	85;	Conservative	57;	Mismatches	155;	Indels	151;
Gaps							
QY	4	SOPMSNHKESTSEDDSTEDVIDKEDIPKVEYVSGSELTTPMAFLOGLSNGMLMQFSQQS	63				
DB	40	TDPGNW-----	EGVKCKMKGRVSKLVLENLNSGSLNGSKSLNQLDQLR	82			
QY	64	VLREMMLODIQOANILP-----	KLENNIGGYCFSWLDEPPKSLM---	105			
DB	83	VL-----	SFKGNSLGSIPNLSGLVNLKSLYLNDNNFSG-----	EFPESLTSLH	126		
QY	106	-----	MYSIPLNKLYIRMKNAFNDVQ-----	FKSKPIQIPLN---	LRVLCFNSDV	149	
DB	127	RUKTVVLSRNRFSKIPSSLRLSLTYFYVDNLFSSGIP-	PLNQATLRAFFNVSNQQL	184			
QY	150	SA--PYYRCQNHLSVEPLTANNAKMRSELLRSNPNSVYCGNAQGRISERFSVVVPLNM	207				
DB	185	SGHIPPTQALNRFNESSTFDNIALCGDIQNS-----	CNDTGTITSPSAKPAIPVAK	237			
QY	208	SRSVTRSGLRTQTLAPKFWQCNCSIGRKETSLSVFCLEKACGDIVGQHVTHYKICTCPKRD	267				
DB	238	THSRTK-----	LGIISGSI-----	CGILILLLFLILCILLNRK	273		
QY	268	RQDERQNSKKRSYPAAEEDPSKVRRCIAIKTEDTENSRDCCDSSAAEMVNSKTP	327				
DB	274	RSKSKRE--ERRSKRVAESKE-----	AKTAETEGTS-DQKNKRSWE-KESE	317			
QY	328	DGDYELAITCPNKEWLLQSIECNKEAAAEVLN-----					361
DB	318	EGSVGTIVLGRDITVYRWYDMDLLKASAEITGRGLSTGYKVAEMSGFITVVKRLKDAG					377
QY	362	-PNQENLRERHANKLLSKK-----	RAY	382			
DB	378	FPFMDFFKRHHFTLGRKHPNVLPLRAY					405

```

RESULT 12
US-09-345-473E-16
; Sequence 16, Application US/09345473E
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin
; TITLE OF INVENTION: Novel Kinases and Uses Thereof
; FILE REFERENCE: 35800/183781
; CURRENT APPLICATION NUMBER: US/09/345,473E
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 645
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-345-473E-16

```

Query Match	4.98;	Score 98.5;	DB 5;	Length 645;
Best Local Similarity	19.08;	Pred. No. 0.074;		
Matches	85;	Conservative	57;	Mismatches 155; Indels 151; Gaps
QY	4	SOPMSWKESTDESDTEVDIKEDIPKVEYSGSELTTPMAFLQGLNSGNLMQFSQQS	63	
Db	40	TPDCNW-----EGVKCMKGRVSKYVLENLNLSSGLNGKSLNQLDQLR	82	
QY	64	VLREMLQDIOQANTLP-----KLEHNITGGYCFSWLDPEPKSLW---	105	
Db	83	VL-----SFKGNLSGSPINLSGLVNLKSLYLNDNNFSG-----EPFESLTSLH	126	
QY	106	-----MYSIPNLKYIRMKNAFNDVQ---FKSKPIQPLN---LRVFCFSNDV	149	
Db	127	RLKTVTLRNRFSGKIPSSLLRLSLRYTYVDNLFSGSIP--PLNQATLRFNVVSNQL	184	
QY	150	SA---PVYRCNHLHSEPTANNAKMKRESLLIRENPNSVYCGNAQGGISERFSVVVPLNM	207	
Db	185	SCHYPTQALNRFNSESFTDIALCGDQIONS-----CNDTGTITSPSAKPAIPVAK	237	
QY	208	SRSVTRSGLTROTAFKFWCQNSICGRKETSILVFCLEKACGDIVGQHVHIKVICIOPKRD	267	
Db	238	TRSRTK-----LIGTIGSSI-----CGGILILLTLLLCILMRKK	273	
QY	268	RIQDEROLNKKKKSVYPAAEDEPSKVRRCIAIKTDETSNDRCDSDSAEWNVSRT	327	
Db	274	RSKSKRE--ERRSKRVASKE-----AKTAETEGTS-DOKNKRPSWE-KESE	317	
QY	328	DGDYRLAITCPNKKENLLOSIEGMKEAAAEVLRN-----	361	
Db	318	EGSVGTVLFGROITVIVRYTMDLLKASAEITLGRGTLSGYKAVMSGGFIITVKKLKDAG	377	
QY	362	-PNOENLRHRHAKLLSKK-----RAY	382	
Db	378	FRPDEFKRRHIEILGRKHPNLVPLRAY	405	

```

RESULT 13
US-09-609-360C-17
; Sequence 17, Application US/09609360C
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; APPLICANT: Meyers, Rachel
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: Novel Kinases and Uses Thereof
; FILE REFERENCE: MP11999-096CP2
; CURRENT APPLICATION NUMBER: US/09/609,360C
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/562,480
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 09/345,473
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-609-360C-17

```

```

Query Match      4.8%; Score 96; DB 5; Length 604;
Best Local Similarity 20.0%; Pred. No. 0.12;
Matches 83; Conservative 55; Mismatches 119; Indels 158; Gaps 21;

QY 38 SELTPEPAFLQGLNSLNMQFSQSVLRMMQLDIOIQANTL----PKL----- 83
      | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 34 SKLVLEYLNTLGTSLNEKSLNQLDQLRVL-----SFRANSLGSGIPNLSCLVNLSKVY 85
      | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 84 --ENINIGGYCFSMVLDEPPKSLMWYSIPLNKL-----YIRMKAKFNVDVQ---FKSK 131
      | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

Db 86 LNDNFGDPFESLTLRLKTLFSG---NRLSGRIPSSLLRLSRLTYLNVEDNLFSG 142
QY 132 MPTQPLN---LRVFLCFSNDVSAVVRQCNHLSVEPLTANNKMRSLRSENPNVSYCG 188
Db 143 IP--PLNQTSRYFNWNNKLSGQI-----PLTRALKQFDES---SFTGNVALCG 187
QY 189 NAQKKGISERFSVVVPLNMSRVSRTSLTRQTLAFKVCQNSCIGRKETSLSVFLCCKACG 248
Db 188 DQIGKEQSELIGII-----AG 203
QY 249 DIVGQHVHVKICT---CPKRDRIQDERQLNSKKRKSVPAAEEDPSKVRRCIAKTE 304
Db 204 SVAGGVVLVILLTLTLLVWCWRRKR-RNQAPREDRKGKGAIAE-----GATTA 250
QY 305 DTESNDRDCDDSAEWNVSRTPDGDIYRLAI---TCPNKEWLLQ-SIEGMIKEAAAEVL- 359
Db 251 ETERDIER--KDRGFSW--ERGEAGVGTLYFLGTSDSEIVRYTMTEDLLK-ASAETLG 305
QY 360 -----RNPQENLRHANKLSLKK-----RAY 382
Db 306 RGTLSGTYKAVMESGFIVTVKRLKNARYPRMEEFKRHVILQLKHPNLVPLRAY 360
RESULT 14
US-09-345-473E-17
; Sequence 17, Application US/09345473E
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin
; TITLE OF INVENTION: Novel Kinases and Uses Thereof
; FILE REFERENCE: 35800/183781
; CURRENT APPLICATION NUMBER: US/09/345,473E
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-345-473E-17
Query Match 4.8%; Score 96; DB 5; Length 604;
Best Local Similarity 20.0%; Pred. No. 0.12;
Matches 83; Conservative 55; Mismatches 119; Indels 158; Gaps 21;
QY 38 SELTTEPMALQGLNSGLNQSQSVLRMMLQDIOIQANTL---PKL----- 83
Db 34 SKLYEYLNLTGSLNEKSLNQDLQRLV-----SFRANSLSGISPLNSGLVNLKSVY 85
QY 84 --ENHNTGGYCFSMVLDEPPKSLMYSIPLNKL-----YIRMKAFNVDVQ---FKSK 131
Db 86 LNDNFGDPFESLTLRLKTLFSG---NRLSGRIPSSLLRLSRLTYLNVEDNLFSG 142
QY 132 MPTQPLN---LRVFLCFSNDVSAVVRQCNHLSVEPLTANNKMRSLRSENPNVSYCG 188
Db 143 IP--PLNQTSRYFNWNNKLSGQI-----PLTRALKQFDES---SFTGNVALCG 187
QY 189 NAQKKGISERFSVVVPLNMSRVSRTSLTRQTLAFKVCQNSCIGRKETSLSVFLCCKACG 248
Db 188 DQIGKEQSELIGII-----AG 203
QY 249 DIVGQHVHVKICT---CPKRDRIQDERQLNSKKRKSVPAAEEDPSKVRRCIAKTE 304
Db 204 SVAGGVVLVILLTLTLLVWCWRRKR-RNQAPREDRKGKGAIAE-----GATTA 250
QY 305 DTESNDRDCDDSAEWNVSRTPDGDIYRLAI---TCPNKEWLLQ-SIEGMIKEAAAEVL- 359
Db 251 ETERDIER--KDRGFSW--ERGEAGVGTLYFLGTSDSEIVRYTMTEDLLK-ASAETLG 305
QY 360 -----RNPQENLRHANKLSLKK-----RAY 382
Db 306 RGTLSGTYKAVMESGFIVTVKRLKNARYPRMEEFKRHVILQLKHPNLVPLRAY 360

RESULT 15
US-09-816-028A-17
; Sequence 17, Application US/09816028A
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/09/816,028A
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: beta-1,4 N-acetylgalactosaminyl (GalNAc)
; OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a)
; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus
US-09-816-028A-17

Query Match 4.6%; Score 91.5; DB 5; Length 347;
Best Local Similarity 22.5%; Pred. No. 0.14;
Matches 46; Conservative 31; Mismatches 62; Indels 65; Gaps 9;

QY 24 DIKEDIPTVEVSCSELTPTEPMALQGLNSGLNQSQSVL-----R 66
Db 77 DEKSKDKPS-----PLNPWAFIRVKNENAITLKASLESILPAIQGVIGYNDCTDGE 128
QY 67 EMLQO-----DIQIQANTLPKLENNHIGGYCFSMVLDEPPKSLMYSIPL 111
Db 129 EILLEFCQKQPSFIPIKYPEIQON---PKSEENKLYSY-YNVASFIPKDEWLKIDV 184
QY 112 NKLY--IRMKAFNV-----DVQFKSKMPIQLNLRVFLCFSNDVSAVVRQCNHLSVEP 164
Db 185 DHYDAAKLYKSFYIPKNKYDVVYSRVDIHYFNDNFCLCKDNN-----GNILKEP 235
QY 165 -----LTANNAKMRESLLRSENP 183
Db 236 GDCLLINNYNLKWEVLIDRINN 259

Search completed: November 16, 2001, 15:56:05
Job time: 437 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 16, 2001, 15:03:33 ; Search time 50.08 seconds
(without alignments)
466.059 Million cell updates/sec

Title: US-09-524-101-2
Perfect score: 2008
Sequence: 1 MYTSQPMWHKSTSEDDSDS.....NLRHANKLLSLKKRAVELP 385

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /SIDSL/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2008	100.0	385	21 AAB00119	DMP53 tumour suppressor
2	300.5	15.0	354	21 AAB00120	CFBP53 tumour suppressor
3	247.5	12.3	350	21 AAB00121	TRIP-AP53 tumour suppressor
4	194	9.7	636	21 AAY50999	Human p73 protein.
5	191	9.5	499	18 AAW36190	Human p53 tumour suppressor
6	191	9.5	499	21 AAY44635	Human p73 beta spl
7	191	9.5	635	20 AAW30661	Human NBS-1 alpha
8	191	9.5	636	18 AAW36184	Human p53 tumour suppressor
9	191	9.5	636	21 AAY44634	Human p73 alpha spl
10	190	9.5	499	18 AAW36183	Monkey p53 tumour suppressor
11	190	9.5	637	18 AAW36182	Monkey p53 tumour suppressor

12	186	9.3	448	20 AAY45246	Human p51 protein
13	186	9.3	448	20 AAY05955	Human cell regulat
14	186	9.3	448	21 AAB11359	Human p63 protein
15	186	9.3	516	20 AAY05954	Human cell regulat
16	186	9.3	516	21 AAB11363	Human p63 protein
17	186	9.3	641	20 AAY45247	Human p51 protein
18	186	9.3	641	20 AAY05953	Human cell regulat
19	186	9.3	641	21 AAB11358	Human p63 protein
20	186	9.3	680	21 AAB11361	Human p63 protein
21	186	9.3	680	21 AAY50997	Human KET protein.
22	185	9.2	680	20 AAY05958	Human cell regulat
23	183	9.1	680	21 AAY50998	Rat KET protein.
24	182	9.1	461	20 AAY05963	Mouse cell regulat
25	182	9.1	586	20 AAY05962	Mouse cell regulat
26	181	9.0	483	20 AAY05961	Mouse cell regulat
27	179	8.9	586	20 AAY41032	Human lung tumor a
28	179	8.9	586	21 AAB11317	Human lung cancer-
29	178	8.9	356	20 AAY43135	Human p40 protein
30	178	8.9	356	21 AAB11360	Human p63 protein
31	178	8.9	389	20 AAY05964	Mouse cell regulat
32	178	8.9	393	20 AAY05957	Human cell regulat
33	178	8.9	461	21 AAB11362	Human p63 protein
34	178	8.9	586	20 AAY05956	Human cell regulat
35	178	8.9	586	21 AAB11357	Human p63 protein
36	171	8.5	506	18 AAW36188	Human p53 tumour s
37	171	8.5	587	18 AAW36187	Human p53 tumour s
38	171	8.5	588	18 AAW36189	Human p53 tumour s
39	170.5	8.5	390	19 AAW37998	Amino acid sequenc
40	168.5	8.4	390	19 AAW37997	Amino acid sequenc
41	168.5	8.4	390	21 AAY0786	Murine tumour-asso
42	167.5	8.3	390	17 AAW02623	Mouse p53 protein.
43	167.5	8.3	390	19 AAW48659	Amino acid sequenc
44	166.5	8.3	370	18 AAW13957	Chimeric p53 prote
45	165	8.2	589	18 AAW36185	Mouse p53 tumour s

ALIGNMENTS

RESULT 1
AAB00119
ID AAB00119 standard; Protein: 385 AA.
XX
AC AAB00119;
XX
DT 08-FEB-2001 (first entry)
XX
DE DMP53 tumour suppressor polypeptide.
XX
KW p53; tumour suppressor gene; insect; phenotype; metazoan;
KW invertebrate; screening; pharmaceutical; pesticide; mis-expression;
KW mutation; modulation.
XX
OS Drosophila melanogaster.
XX
PN W0200055178-A1.
XX
PD 21-SEP-2000.
XX
PF 13-MAR-2000; 2000WO-US06602.
XX
PR 16-MAR-1999; 99US-0268969.
XX
PR 23-FEB-2000; 2000US-0184373.
XX
PA (EXEL-) EXELIX INC.
XX
PI Buchman AR, Platt DM, Ollman MM, Young LM, Demsky MR, Keegan KP;
PI Friedman L, Koczynski C, Larson JS, Robertson SA;
XX
XX WPI; 2000-638178/61.
DR N-PSDB; AAA53973.
XX
PT Novel p53 tumor suppressor gene encoding a protein useful for

PT genetically modifying metazoan invertebrate organisms, such as insects
 for screening compounds of pharmaceutical use or a pesticide

XX Claim 14; Page 70-71; 98pp; English.

CC Insect p53 tumour suppressor genes can be used to genetically modify
 CC metazoan invertebrate organisms, such as insects and worms, or
 CC cultured cells, resulting in p53 expression or mis-expression. The
 CC tumour suppressor genes, a p53 polypeptide or genetically modified
 CC organisms or cells are used in screening assays to identify compounds
 CC or molecules, preferably a pharmaceutical agent or a pesticide, that
 CC modulates p53 activity. The genetically modified organisms or cells
 CC are also useful for studying p53 activity by detecting the phenotype
 CC caused by the expression or mis-expression of the p53 protein in the
 CC insect. The method additionally comprises observing a second insect
 CC having the same genetic modification as the previous one, which
 CC causes the expression or mis-expression of the p53 protein, where the
 CC second animal additionally comprises a mutation in a desired gene and
 CC differences between the phenotype of the first and second identifies
 CC the desired gene as capable of modifying the function of the gene
 CC encoding the p53 protein. The genetically modified organisms or
 CC cells are also useful for identifying other genes modulating the
 CC function of, or interaction with the p53 gene.

XX Sequence 385 AA;

Query Match 100.0%; Score 2008; DB 21; Length 385;

Best Local Similarity 100.0%; Pred. No. 3.9e-203;

Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYISQPMWHKSTEDSDSTEDVDIKEDIPKTVESGSELTPMFAFLOGLNSGNLMQFS 60

DB 1 MYISQPMWHKSTEDSDSTEDVDIKEDIPKTVESGSELTPMFAFLOGLNSGNLMQFS 60

QY 61 QGVLRNEMMLQDIQIANTPLKLENNHNGGVCFSWLDPEPKSLMYSIPLNKLIRMNK 120

DB 61 QGVLRNEMMLQDIQIANTPLKLENNHNGGVCFSWLDPEPKSLMYSIPLNKLIRMNK 120

QY 121 AFNVDFVQFKSMPTQPLNLRVFLCFSDNSVAPVVRCONHLSVEPLTANNAMRESLLRSE 180

DB 121 AFNVDFVQFKSMPTQPLNLRVFLCFSDNSVAPVVRCONHLSVEPLTANNAMRESLLRSE 180

QY 181 NPNSVYCGNAGGKISERFSVVPVPLNMSRSTRGLTRQTLAFKFCVQNSCIGRKETSLV 240

DB 181 NPNSVYCGNAGGKISERFSVVPVPLNMSRSTRGLTRQTLAFKFCVQNSCIGRKETSLV 240

QY 241 FCLEKACGDIVGQVTHVKTCTPRDRIDQEROLNSKKKSVPEAAEDEPSKVRCA 300

DB 241 FCLEKACGDIVGQVTHVKTCTPRDRIDQEROLNSKKKSVPEAAEDEPSKVRCA 300

QY 301 IKTEDESNDSDCDSDAAEWNVSRTPDGYRLAITCPNKEWLLQSGMKEAAAEVLR 360

DB 301 IKTEDESNDSDCDSDAAEWNVSRTPDGYRLAITCPNKEWLLQSGMKEAAAEVLR 360

QY 361 NPQENLRHANKLLSLKRAYELP 385

DB 361 NPQENLRHANKLLSLKRAYELP 385

RESULT 2

ID AAB00120

XX AAB00120 standard; Protein; 354 AA.

AC AAB00120;

XX AAB00120;

DT 08-FEB-2001 (first entry)

XX CPBp53 tumour suppressor polypeptide.

XX p53; tumour suppressor gene; insect; phenotype; metazoa;

KW invertebrate; screening; pharmaceutical; pesticide; mis-expression;

KW mutation; modulation.

KW

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Leptinotarsa decemlineata.

WO200055178-A1.

11-SEP-2000.

13-MAR-2000; 2000WO-US06602.

16-MAR-1999; 99US-0268969.

23-FEB-2000; 2000US-0184373.

(EXEL-) EXELIXIS INC.

Buchman AR, Platt DM, Ollman MM, Young LM, Demsky MR, Keegan KP;

Friedman L, Koczynski C, Larson JS, Robertson SA;

WPI; 2000-638178/61.

N-PSDB; AAA53974.

Novel p53 tumor suppressor gene encoding a protein useful for

genetically modifying metazoan invertebrate organisms, such as insects

for screening compounds of pharmaceutical use or a pesticide

Claim 14; Page 73-74; 98pp; English.

Insect p53 tumour suppressor genes can be used to genetically modify

metazoan invertebrate organisms, such as insects and worms, or

cultured cells, resulting in p53 expression or mis-expression. The

tumour suppressor genes, a p53 polypeptide or genetically modified

organisms or cells are used in screening assays to identify compounds

or molecules, preferably a pharmaceutical agent or a pesticide, that

modulates p53 activity. The genetically modified organisms or cells

are also useful for studying p53 activity by detecting the phenotype

caused by the expression or mis-expression of the p53 protein in the

insect. The method additionally comprises observing a second insect

having the same genetic modification as the previous one, which

causes the expression or mis-expression of the p53 protein, where the

second animal additionally comprises a mutation in a desired gene and

differences between the phenotype of the first and second identifies

the desired gene as capable of modifying the function of the gene

encoding the p53 protein. The genetically modified organisms or

cells are also useful for identifying other genes modulating the

function of, or interaction with the p53 gene.

Sequence 354 AA;

Query Match 15.0%; Score 300.5; DB 21; Length 354;

Best Local Similarity 28.5%; Pred. No. 5.7e-23;

Matches 103; Conservative 60; Mismatches 122; Indels 77; Gaps 18;

QY 45 MAPFLOGNSGNLMQFSQSVLRNEMMLQDI---QIQAN-----TLPLKLNH 86

DB 17 laemegdmhlnffkdeplndlnysnlngslvsnldskmhllfpgvqtvspsndey 76

QY 87 NIGGCFNSVLDEPP---KSLMYSIPLNKLIRNKAFFNVDFVQFSKMPQIPLMLRVEL 143

DB 77 d-gpyefe--vdvhtpvakuswystlnkvytmngspfvdfvr-shrrppplfir--- 129

QY 144 CFSNDV-SAP-----VVRCONHLSVEPLTANNNAK--MRESLLRSENPNVSVGNAQSGK 194

DB 130 --stpvysapqfaqecvrcylrhfnshkesdglkehlrphircanqyaaylgd---ks 184

QY 195 ISERSVVPVPLNMSRSTRGLTRQTLAFKFCVQNSC-----IGRKETSLVFLCERACGDI 250

DB 185 knerlsvvpfipgltgtes--vre--ifefvcknscpsgmnraraveifltednqgti 240

QY 251 VGOHVLHVKTCTPRDRIDQEROLNSKKKSVPEAAEDEPSKVR 296

DB 241 ygrkclnrvicscpkrdekdekdtantnlphgkkrkmeqskkpmgtgaend-tkeft 299

QY 297 RCIAKTEDESNDSDCDSDAAE---WNVSRTPDGYRLAITCPNKEWLLQSGMKE 353

CC suppressor, particularly in tumors where an alteration in the wild-type

CC p53 allele has not been identified. (I) and (II) may also be used for
 CC development of specific cytotoxic agents and for predicting the risk of
 CC developing cancer. This sequence represents the human p73 protein
 CC described in the method of the invention.

XX Sequence 636 AA;
 SQ
 Query Match 9.7%; Score 194; DB 21 Length 636;
 Best Local Similarity 23.9%; Pred. No. 2.6e-11;
 Matches 78; Conservative 48; Mismatches 142; Indels 58; Gaps 12;
 QY 17 EDDSTEVDIKEDIPKTVFVSGSELTTEPMAPLOGLSNGLMDFSQSVLRMLQ----- 71
 Db 23 epdstyfdlpqssrgnnevvgtdssmdvfhlegmttsvmagfnllsstmdqmsraasa 82
 QY 72 -----DIOIQANTLPKLEHNHNGGYCFSWVLDE---PPKSL 104
 Db 83 spytpehaasvthpsyaqpsstfdtmspapvpsntdyp-gphhfevtfgqstaksat 141
 QY 105 WMYSIPLNKLKLYIRMNKAFNVDQFKSMPIQP-LNLRFVLCF--SNDVSAFVVRCONHLS 161
 Db 142 wtyspllklycqiak--tcpiqikvstppppgiarampvykka-hvtadvvkrcphel 199
 QY 162 VEPLTANNAKMRESLRSNP-SVYCGNAQGGKISERFSVSVVPLNMSRSVTRSGLTRQT 220
 Db 200 grdfnegqsapashlirvegnnlsqyvddp---vtgrqsvvvpv---epqvgvteftt 251
 QY 221 LAFKFCVQNSCIG---RKETSIVFCLEKACGDIVGQHVHVKICTCPKRDRIODE----- 272
 Db 252 ilynfmcnssvcvgmarrpiliitlenrdqvgvlgrrsfegricacpgrdrkadedhyre 311
 QY 273 -ROLN--SKRRKSVPEAAEEDPSKV 295
 Db 312 qqalnessakngaaskrafkspav 337

RESULT 5

AAW36190
 ID AAW36190 standard; Protein; 499 AA.
 XX
 AC AAW36190;
 XX
 DT 27-APR-1998 (first entry)
 XX
 DE Human p53 tumour suppressor-related protein S. p70b.
 XX
 KW SR-p70; human; transcription factor; p53; tumour suppressor gene;
 KW homology; differential splicing; diagnosis; cancer; neuroblastoma;
 KW gene therapy; apoptosis.
 XX
 OS Homo sapiens.
 XX
 PN W09728186-AL.
 XX
 PD 07-AUG-1997.
 XX
 PF 03-FEB-1997; 97WO-FR00214.
 XX
 PR 02-FEB-1996; 96FR-0001309.
 XX
 PA (SNFI) SANOFI SA.
 XX
 PI Caput D, Ferrara P, Kaghad AM;
 XX
 XX WPI; 1997-402550/37.
 DR N-ESDB; AAV01505.
 XX
 PT New polypeptide(s) encoded by the SR-p70 tumour suppressor gene -
 PT and related nucleic acid, useful for diagnosis and treatment of
 PT tumours
 XX
 XX Claim 1; Page 72-73; 136pp; French.

XX This is the amino acid sequence of the human protein SR-p70b. SR-p70
 CC are transcription factors which may control the activity of
 CC p53-regulated genes, and are expressed by tumour suppressor genes related
 CC to the p53 gene family. The gene sequence was isolated from the human
 CC neuroblastoma cell line SK-N-SH, using primers AAV01515 and AAV01519.
 CC The SR-p70b gene sequence contains a 94 bp deletion between bases
 CC 1516-1517 as compared to the SR-p70a sequence (AAV01498). This deletion
 CC causes a reading frame shift resulting in the generation of a stop codon
 CC at position 1498-1500. The resultant protein is truncated by 137 amino
 CC acids as compared to the SR-p70a protein (AAW36184). The sequence can be
 CC used in the diagnosis and monitoring of cancer, especially neuroblastoma.
 CC The nucleic acid sequences and corresponding antisense sequences, are
 CC also useful in gene therapy, e.g. to regulate apoptosis.

XX Sequence 499 AA;

Query Match 9.5%; Score 191; DB 18; Length 499;
 Best Local Similarity 23.9%; Pred. No. 3.7e-11;
 Matches 78; Conservative 47; Mismatches 143; Indels 58; Gaps 12;
 QY 17 EDDSTEVDIKEDIPKTVFVSGSELTTEPMAPLOGLSNGLMDFSQSVLRMLQ----- 71
 Db 23 epdstyfdlpqssrgnnevvgtdssmdvfhlegmttsvmagfnllsstmdqmsraasa 82
 QY 72 -----DIOIQANTLPKLEHNHNGGYCFSWVLDE---PPKSL 104
 Db 83 spytpehaasvthpsyaqpsstfdtmspapvpsntdyp-gphhfevtfgqstaksat 141
 QY 105 WMYSIPLNKLKLYIRMNKAFNVDQFKSMPIQP-LNLRFVLCF--SNDVSAFVVRCONHLS 161
 Db 142 wtyspllklycqiak--tcpiqikvstppppgiarampvykkaehvtdvdkrcphel 199
 QY 162 VEPLTANNAKMRESLRSNP-SVYCGNAQGGKISERFSVSVVPLNMSRSVTRSGLTRQT 220
 Db 200 grdfnegqsapashlirvegnnlsqyvddp---vtgrqsvvvpv---epqvgvteftt 251
 QY 221 LAFKFCVQNSCIG---RKETSIVFCLEKACGDIVGQHVHVKICTCPKRDRIODE----- 272
 Db 252 ilynfmcnssvcvgmarrpiliitlenrdqvgvlgrrsfegricacpgrdrkadedhyre 311
 QY 273 -ROLN--SKRRKSVPEAAEEDPSKV 295
 Db 312 qqalnessakngaaskrafkspav 337

RESULT 6

AAW44635
 ID AAW44635 standard; Protein; 499 AA.
 XX
 AC AAW44635;
 XX
 DT 07-APR-2000 (first entry)
 XX
 DE Human p73 beta splice variant protein.
 XX
 KW p73; splice variant; human; p73 beta; p53 tumour suppressor;
 KW E6; oncoprotein; inhibitor; apoptosis; human papilloma virus; HPV;
 KW cancer; uterine cervix; anogenital; oesophageal squamous cell;
 KW laryngeal papilloma; bronchiolo-alveolar; penile; bladder; carcinoma.
 XX
 OS Homo sapiens.
 XX
 PN W09966946-AL.
 XX
 PD 29-DEC-1999.
 XX
 PF 23-JUN-1999; 99WO-US14057.
 PR 24-JUN-1998; 98US-0090526.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.

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XX El-Deiry WS;
XX PI
XX WPI: 2000-136954/12.
XX N-PSDB: AAZ49690.
XX Novel methods using p73 to induce apoptosis in E6- expressing cells
XX used to treat Human papillomavirus induced cancers
XX Claim 12; Page 42-43; 45pp; English.
XX The present sequence is a human p73 beta protein, which is a splice
XX variant of p73. p73 is a homolog of p53 tumour suppressor, capable of
XX arresting the growth of E6 protein-expressing cells. It is not targeted
XX for degradation by E6 oncoprotein and has been found to be a potent
XX inhibitor of cancer colony growth and inducer of apoptosis. Apoptosis
XX can be induced in E6-expressing cells, by administering p73 protein or a
XX DNA construct encoding p73. It can be used to treat human papilloma
XX virus (HPV) infections, cancers of the uterine cervix, anogenital,
XX oesophageal squamous cell cancer, laryngeal papilloma, and
XX bronchiolo-alveolar, penile and bladder carcinoma.
XX Sequence 499 AA;

Query Match 9.5%; Score 191; DB 21; Length 499;
Best Local Similarity 23.9%; Pred. No. 3.7e-11;
Matches 78; Conservative 47; Mismatches 143; Indels 58; Gaps 12;

QY 17 EDDSTEVDIKEDIPKTVVSGSELTTEPMFQLGNSGLNQFQQSVLRMMQLQ----- 71
  ||| | : : : : : : : : : : : : : : : : : : : : : : : :
Db 23 epdstyfdlpqssrgnnevvgtdssmdvfhlegmttsvmaqfnllsstmdqmsraasa 82
  ||| | : : : : : : : : : : : : : : : : : : : : : : : :
QY 72 -----DIQIQANTLPKLENNHNGGVCFSMWLDE---PPKSL 104
  ||| | : : : : : : : : : : : : : : : : : : : : : : : :
Db 83 spytpehaasvthspyaqpsstfdtmspavipsntdyp-gphhfevtfgqsstaksat 141
  ||| | : : : : : : : : : : : : : : : : : : : : : : : :
QY 105 WMYSLPLNKLIRNMKNFNDVQFKSKMPQIP-LNLRVFLCF--SNDVSAPVVRQNHLS 161
  ||| | : : : : : : : : : : : : : : : : : : : : : : : :
Db 142 wtyspllklycqiaak--tcpigikvstpppgtairampvykkaehvtdvkrpcphel 199
  ||| | : : : : : : : : : : : : : : : : : : : : : : : :
QY 162 VEPLTANNAKMRESLLRSENPN-SVYCGNAQKGISERFSVVVPLNMSRVSRTSLTROT 220
  ||| | : : : : : : : : : : : : : : : : : : : : : : : :
Db 200 grdfneqgsapashlirvegnnlsgyvddp----vtgrqsvvpy----epqvgteftt 251
  ||| | : : : : : : : : : : : : : : : : : : : : : : : :
QY 221 LAFKVCQNSCIG---RKETSLVFLCERACGDIVGQVHVKICTCPKRDRIQDE----- 272
  ||| | : : : : : : : : : : : : : : : : : : : : : : : :
Db 252 ilynfmcnscvvgmnrrpiliitilemrdgqvlgrtsfegracacpgdrkadedhyre 311
  ||| | : : : : : : : : : : : : : : : : : : : : : : : :
QY 273 -ROLN--SKKRKSVPEAAEEDPSKV 295
  ||| | : : : : : : : : : : : : : : : : : : : : : : : :
Db 312 qgalnessakngaaskrafkqspav 337
  ||| | : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
AAW30661
ID AAW30661 standard; Protein; 635 AA.
XX AC AAW30661;
XX DT 07-APR-1999 (first entry)
XX DE Human NBS-1 alpha protein.
XX KW Human; NBS-1; p73; antibody; p53 responsive element; p53 promoter;
XX KW p53-dependent tumour; growth inhibition.
XX OS Homo sapiens.
XX PN WC09851350-A1.
XX PD 19-NOV-1998.
XX

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PF 12-MAY-1998; 98WO-US09516.
XX PR
XX 12-MAY-1997; 97US-0046207.
XX PA (DAND ) DANA FARBER CANCER INST INC.
XX PI Jost C, Kaelin W;
XX DR WPI: 1999-059690/05.
XX PT Treating subjects using NBS-1 proteins and antibodies - used to
XX interact with p53-responsive genes and inhibit growth of
XX p53-dependent tumour cells
XX PS Example; Fig 1A; 65pp; English.
XX CC A method has been developed for treating a subject having a
XX p53-dependent tumour cell. The method comprises: (a) determining the
XX level of NBS-1 protein (also known as p73) expressed in the tumour
XX cell and in a corresponding non-malignant cell; (b) selecting subjects
XX having NBS-1 protein level comparable or below that in a corresponding
XX normal cell; (c) elevating tumour cell NBS-1 level, where NBS-1
XX interacts with p53-responsive promoters. Also described in the present
XX invention is an antibody that specifically binds to NBS-1, and an
XX antibody raised to the carboxy portion of NBS-1. NBS-1 can activate the
XX transcription of p53-responsive genes and can inhibit cell growth in a
XX p53-like manner. The present sequence represents the human NBS-1 alpha
XX protein from the present invention.
XX Sequence 635 AA;

Query Match 9.5%; Score 191; DB 20; Length 635;
Best Local Similarity 23.9%; Pred. No. 5.4e-11;
Matches 78; Conservative 47; Mismatches 143; Indels 58; Gaps 12;

QY 17 EDDSTEVDIKEDIPKTVVSGSELTTEPMFQLGNSGLNQFQQSVLRMMQLQ----- 71
  ||| | : : : : : : : : : : : : : : : : : : : : : : : :
Db 23 epdstyfdlpqssrgnnevvgtdssmdvfhlegmttsvmaqfnllsstmdqmsraasa 82
  ||| | : : : : : : : : : : : : : : : : : : : : : : : :
QY 72 -----DIQIQANTLPKLENNHNGGVCFSMWLDE---PPKSL 104
  ||| | : : : : : : : : : : : : : : : : : : : : : : : :
Db 83 spytpehaasvthspyaqpsstfdtmspavipsntdyp-gphhfevtfgqsstaksat 141
  ||| | : : : : : : : : : : : : : : : : : : : : : : : :
QY 105 WMYSLPLNKLIRNMKNFNDVQFKSKMPQIP-LNLRVFLCF--SNDVSAPVVRQNHLS 161
  ||| | : : : : : : : : : : : : : : : : : : : : : : : :
Db 142 wtyspllklycqiaak--tcpigikvstpppgtairampvykkaehvtdvkrpcphel 199
  ||| | : : : : : : : : : : : : : : : : : : : : : : : :
QY 162 VEPLTANNAKMRESLLRSENPN-SVYCGNAQKGISERFSVVVPLNMSRVSRTSLTROT 220
  ||| | : : : : : : : : : : : : : : : : : : : : : : : :
Db 200 grdfneqgsapashlirvegnnlsgyvddp----vtgrqsvvpy----epqvgteftt 251
  ||| | : : : : : : : : : : : : : : : : : : : : : : : :
QY 221 LAFKVCQNSCIG---RKETSLVFLCERACGDIVGQVHVKICTCPKRDRIQDE----- 272
  ||| | : : : : : : : : : : : : : : : : : : : : : : : :
Db 252 ilynfmcnscvvgmnrrpiliitilemrdgqvlgrtsfegracacpgdrkadedhyre 311
  ||| | : : : : : : : : : : : : : : : : : : : : : : : :
QY 273 -ROLN--SKKRKSVPEAAEEDPSKV 295
  ||| | : : : : : : : : : : : : : : : : : : : : : : : :
Db 312 qgalnessakngaaskrafkqspav 337
  ||| | : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8
AAW36184
ID AAW36184 standard; Protein; 636 AA.
XX AC AAW36184;
XX DT 27-APR-1998 (first entry)
XX DE Human p53 tumour suppressor-related protein SR-p70a.
XX KW SR-p70; human; transcription factor; p53; tumour suppressor gene;
XX KW homology; differential splicing; diagnosis; cancer; neuroblastoma;

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KW gene therapy; apoptosis.
 XX Homo sapiens.
 OS WO9728186-A1.
 PN 07-AUG-1997.
 PD 03-FEB-1997; 97WO-FR00214.
 PF 02-FEB-1996; 96FR-0001309.
 PR (SNFI) SANOFI SA.
 XX Caput D, Ferrara P, Kaghad AM;
 PI WPI: 1997-402550/37.
 DR N-PSDB; AAV01498.
 XX New polypeptide(s) encoded by the SR-p70 tumour suppressor gene -
 PT and related nucleic acid, useful for diagnosis and treatment of
 PT tumours
 PT Claim 7; Fig 6; 136pp; French.
 PS CC This is the amino acid sequence of the human protein SR-p70a. SR-p70
 CC are transcription factors which may control the activity of
 CC p53-regulated genes, and are expressed by tumour suppressor genes related
 CC to the p53 gene family. The gene sequence was isolated from the human
 CC colon adenocarcinoma cell line HT-29, using primers AAV01506-7. The
 CC sequence can be used in the diagnosis and monitoring of cancer,
 CC especially neuroblastoma. The nucleic acid sequences and corresponding
 CC antisense sequences, are also useful in gene therapy, e.g. to regulate
 CC apoptosis.
 XX Sequence 636 AA;
 SQ
 Query Match 9.5%; Score 191; DB 18; Length 636;
 Best Local Similarity 23.9%; Pred. No. 5.5e-11;
 Matches 78; Conservative 47; Mismatches 143; Indels 58; Gaps 12;
 QY 17 EDDSTEVDIKEDIPKTVESGSELTTEPMFLQGLNSGNLMQFSQSVLRMMQLQ----- 71
 Db 23 epdstyfdlpqssrgnnevvgtdssmdvfhlegmttsvmaqfnllsstmdqmsraasa 82
 QY 72 -----DIQIQANTLPKLENNHIGGYCFSMVLDE---PPKSL 104
 Db 83 spytpehaasvthspagpsstfdtmspapvpsntdyp-gphhfevtfqgsstaksat 141
 QY 105 WMYSIPLNKLYIRMKAFNVDYQFSKRMPIQP-LNLRVFLCF--SNDVSAPVVRCONHLS 161
 Db 142 wtyspllkkllycqlak--Lcpikqvstpppgptairampvykkaehvtdvkrpcphel 199
 QY 162 VEPLTANNKMRSLRSENPN-SVYCGNAGKGISERFSVVVPLNMSRVSRTSLTRQT 220
 Db 200 grdfneqgsapashlirvegnlnsqyvdpp-----vtgrqsvvpy-----epqvgteftt 251
 QY 221 LAFKFCVQNSCIG---RKETSIVFLCEKACGDIVGQHVHVICTCPKRDRIQDE----- 272
 Db 252 ilynfmcnscvsgmmrrpiliitiilemrdqvgvlgrrsfegricacpgrdrkadedhyre 311
 QY 273 -RQLN--SKRRKSVPEAAFEDEPSKV 295
 Db 312 qgalnessakngaskrafkqspav 337
 RESULT 9
 AAY44634
 ID AAY44634 standard; Protein; 636 AA.
 XX
 AC AAY44634;
 XX

DT 07-APR-2000 (first entry)
 XX Human p73 alpha splice variant protein.
 DE
 XX p73; splice variant; human; p73 alpha; p53 tumour suppressor;
 KW E6; oncoprotein; inhibitor; apoptosis; human papilloma virus; HPV;
 KW cancer; uterine cervix; anogenital; oesophageal squamous cell;
 KW laryngeal papilloma; bronchiolo-alveolar; penile; bladder; carcinoma.
 XX Homo sapiens.
 OS WO9966946-A1.
 PN 29-DEC-1999.
 PD 23-JUN-1999; 99WO-US14057.
 PF 24-JUN-1998; 98US-0090526.
 PR (UYPE-) UNIV PENNSYLVANIA.
 PA El-Deiry WS;
 PI WPI: 2000-136/54/12.
 DR N-PSDB; AAZ49690.
 XX Novel methods using p73 to induce apoptosis in E6- expressing cells
 PT used to treat Human papillomavirus induced cancers
 PT Claim 12; Page 40-41; 45pp; English.
 XX The present sequence is a human p73 alpha protein, which is a splice
 CC variant of p73. p73 is a homolog of p53 tumour suppressor, capable of
 CC arresting the growth of E6 protein-expressing cells. It is not targeted
 CC for degradation by E6 oncoprotein and has been found to be a potent
 CC inhibitor of cancer colony growth and inducer of apoptosis. Apoptosis
 CC can be induced in E6-expressing cells, by administering p73 protein or a
 CC DNA construct encoding p73. It can be used to treat human papilloma
 CC virus (HPV) infections, cancers of the uterine cervix, anogenital,
 CC oesophageal squamous cell cancer, laryngeal papilloma, and
 CC bronchiolo-alveolar, penile and bladder carcinoma.
 XX Sequence 636 AA;
 SQ
 Query Match 9.5%; Score 191; DB 21; Length 636;
 Best Local Similarity 23.9%; Pred. No. 5.5e-11;
 Matches 78; Conservative 47; Mismatches 143; Indels 58; Gaps 12;
 QY 17 EDDSTEVDIKEDIPKTVESGSELTTEPMFLQGLNSGNLMQFSQSVLRMMQLQ----- 71
 Db 23 epdstyfdlpqssrgnnevvgtdssmdvfhlegmttsvmaqfnllsstmdqmsraasa 82
 QY 72 -----DIQIQANTLPKLENNHIGGYCFSMVLDE---PPKSL 104
 Db 83 spytpehaasvthspagpsstfdtmspapvpsntdyp-gphhfevtfqgsstaksat 141
 QY 105 WMYSIPLNKLYIRMKAFNVDYQFSKRMPIQP-LNLRVFLCF--SNDVSAPVVRCONHLS 161
 Db 142 wtyspllkkllycqlak--Lcpikqvstpppgptairampvykkaehvtdvkrpcphel 199
 QY 162 VEPLTANNKMRSLRSENPN-SVYCGNAGKGISERFSVVVPLNMSRVSRTSLTRQT 220
 Db 200 grdfneqgsapashlirvegnlnsqyvdpp-----vtgrqsvvpy-----epqvgteftt 251
 QY 221 LAFKFCVQNSCIG---RKETSIVFLCEKACGDIVGQHVHVICTCPKRDRIQDE----- 272
 Db 252 ilynfmcnscvsgmmrrpiliitiilemrdqvgvlgrrsfegricacpgrdrkadedhyre 311
 QY 273 -RQLN--SKRRKSVPEAAFEDEPSKV 295
 Db 312 qgalnessakngaskrafkqspav 337

```

RESULT_10
AAW36183
ID AAW36183 standard; Protein; 499 AA.
XX
AAW36183;
XX
27-APR-1998 (first entry)
XX
XX Monkey p53 tumour suppressor-related protein SR-p70b.
DE
DE
XX
XX SR-p70; monkey; transcription factor; p53; tumour suppressor gene;
XX KW homology; differential splicing; diagnosis; cancer; neuroblastoma;
XX KW gene therapy; apoptosis.
XX
XX Cercopithecus aethiops.
OS
XX
XX W09728186-A1.
PN
XX
XX 07-AUG-1997.
PD
XX
XX 03-FEB-1997; 97WO-FR002114.
XX
XX 02-FEB-1996; 96FR-0001309.
XX
XX (SNFI ) SANOFI SA.
XX
XX Caput D, Ferrara P, Kaghad AM;
PI
XX
XX WPI; 1997-402550/37.
XX
XX N-PSDB; AAV01497.
DR
XX
XX
XX
XX New polypeptide(s) encoded by the SR-p70 tumour suppressor gene -
XX PT and related nucleic acid, useful for diagnosis and treatment of
XX PT tumours
XX
XX Claim 1; Fig 5; 136pp; French.
XX
XX This is the amino acid sequence of the protein SR-p70b from monkey
XX CC cells. SR-p70 are transcription factors which may control the activity
XX CC of p53-regulated genes, and are expressed by tumour suppressor genes
XX CC related to the p53 gene family. The gene sequence was isolated from a
XX CC cDNA library by sequencing the inserts and comparing to sequence
XX CC databases. The protein sequence contains regions of homology to the p53
XX CC protein. The SR-p70b gene sequence was isolated simultaneously with the
XX CC SR-p70a sequence (AAV01496) from the library and is created by
XX CC differential splicing of the SR-p70 mRNA sequence. The sequences can be
XX CC used in the diagnosis and monitoring of cancer, especially neuroblastoma.
XX CC The nucleic acid sequences and corresponding antisense sequences, are
XX CC also useful in gene therapy, e.g. to regulate apoptosis.
XX
XX Sequence 499 AA;
SQ

Query Match 9.5%; Score 190; DB 18; Length 499;
Best Local Similarity 23.9%; Pred. No. 4.7e-11;
Matches 78; Conservative 47; Mismatches 143; Indels 58; Gaps 12;

QY 17 EDDSTEVDIKEDIPKTVYSGSELFTPEAPFLQGLASGNLMQFSQSVLREMMIQ----- 71
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 23 epdstyfdlpqsrgrnnevvgtdssmdvfflegmtsvmadfnllstmdqmsraasa 92
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 72 -----DIIQANTLPKLEHNHIGGYCFSMVLDE---PPKSL 104
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 83 spytpehaasvpthsyapgsstfdtmsapvipnsntdyp-gphhfevtfgqsstaksat 141
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 105 WMYSTPLNKLIRMKAFNVDFQSKMPTQP-INLRFVLCF--SNDSYAPVVRCONHLS 161
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 142 wtyspllkkiycqlak--tcpiqikvsappppggtairampvykkaehdvdkrcpnhel 199
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 162 VEPLTANNKMRRESILRSNP--SVYCGNAGKGCISERFSVVVPLNMRSVTRSGLTRQT 220
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 200 grdfnegasapashlirvegnllsryddp-----vtgrgsvvpy-----ppvgvgtftt 251
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

Db 83 spytpehaasvptshpsyaqpsstfdmtspapvipntdyp-gphhfevtfqgskstakst 141
QY 105 WYTSIPLNKLKIRMKAFNVDQFKSQMPLQ-LMLRVFLCF--SNDVSAPVVRQCNHL 161
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 142 wtyspllklyciak--tpiqikvsapppggtairampyykkaehvtdivkrcpnhel 199
QY 162 VEPLTANNAKMRESLLRSENPN-SVYCGNAQKGIGSERFSVVVPLNMSRVSRTSGITROT 220
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 200 grdfneggapashliirvegnisqyvddp---vtgrgsvvpy---eppgvgteftt 251
QY 221 LAFKFCVQNSCIG---RKETSFLVFCLEKAGDVGIOHVIHVKICTCPKRDRIODE----- 272
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 252 ilynfmcnsscvggmrrpiliitletrdgvgigrsfeircacpgrarkadedhyre 311
QY 273 -ROLN--SKKRKSVPEAAEEDPSK 295
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 312 qqalnessakngaaakrfkqspav 337

RESULT 12
AAAY45246
ID AAY45246 standard; Protein: 448 AA.
XX
AC AAY45246;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human p51 protein A.
XX
KW Human: p51; p53 related gene; cell proliferation; regulation; cancer;
KW tumour suppression; diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 1..59
FT /label= transactivation_domain
FT Domain 142..321
FT /label= DNA_binding_domain
FT Domain 353..397
FT /label= oligomerisation_domain
XX
PN WO9950412-A1.
XX
PD 07-OCT-1999.
XX
PF 24-MAR-1999; 99WO-JP01512.
XX
PR 27-MAR-1998; 98JP-0100467.
XX
PA (SAKA ) OTSUKA PHARM CO LTD.
PA (IKAWA/) IKAWA Y.
XX
PI Ikawa Y, Ikawa S, Obinata M;
XX
DR WPI; 1999-591318/50.
DR N-PSDB; AAZ25770.
XX
XX
XX New p53 related human gene p51, useful for diagnosis, investigation and
XX treatment of cancers and screening for potential cell proliferation
XX agents -
XX
XX Claim 1; Page 147-148; 163pp; Japanese.
XX
XX The present sequence represents a human p51 protein, which is related to
XX p53 and has cell proliferation regulation and tumour suppression
XX activity. The p51 gene can be used in the investigation, diagnosis and
XX treatment of diseases such as cancer, with which the p53 family cell
XX proliferation regulation is associated. The p51 protein may be used for
XX screening potential agonists and antagonists of its regulatory function,
XX for use as drugs,
XX
XX Sequence 448 AA;

```

```

Query Match 9.3%; Score 186; DB 20; Length 448;
Best Local Similarity 22.2%; Pred. No. 1e-10;
Matches 75; Conservative 59; Mismatches 124; Indels 80; Gaps 15;

QY 5 QPMSWKHSTDESDST-EVDIKEDIPKTVESGSELATTEPMAFLQGLNSGNLWQFSQOS 63
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 31 qpdlfnfdepsegdgnknielsmd---cirmqdsdl-sdpm-----wpqytnlg 76
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 64 VLREMLQDIOIQ---ANTLPKLENH-----NI 88
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 77 llnsm---dqgiqngssstspyntdhagnsvtapspyaqpsstfdalspsaipntdyp 133
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 89 GGYCFSMVLDE---PPKSLWMSIPLNKLKIRMKAFNVDQFKSQMPLQ-LMLRVFLCF 145
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 134 gphsfdivsqgstakstakstwtstlkklyciaktcpiqikvmtcppp-gqavirampvy 192
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 146 --SNDVSAPVVRQCNHL-SVEPLTANNAKMRESLLRSENPN-SVYCGNAQKGISE-----RF 199
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 193 kkaehvtevvkrcpnhelshrefnegqiappshliirve-----gnshaqyvedpitgrq 245
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 200 SVVPLNMSRVSRTSGITROT-LAFKFCVQNSCIG---RKETSFLVFCLEKAGDVGIOHVI 256
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 246 svlvpy---eppgvgtefttvltnfmcnsscvggmrrpiliitletrdgvgigrf 301
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 257 HVKICTCPKRDRIQDERQLNSKKRKSVPPEAAEEDPSK 294
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 302 earicacpgrdrkade---dsirkqvsdstkngdgtk 336
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 13
AAAY05955
ID AAY05955 standard; Protein: 448 AA.
XX
AC AAY05955;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cell regulatory protein p63, isoform huTAp63 gamma.
XX
KW Cell regulatory protein; p63; huTAp63 gamma; TA63 gamma; human;
KW cancer; tumour suppressor; cell cycle control; apoptosis;
KW cell proliferation; cell differentiation; therapy.
XX
OS Homo sapiens.
XX
PN WO9919357-A2.
XX
PD 22-APR-1999.
XX
PF 02-OCT-1998; 98WO-US21992.
XX
PR 29-MAY-1998; 98US-0087216.
PR 15-OCT-1997; 97US-0062076.
XX
PA (HARD ) HARVARD COLLEGE.
XX
PI McKeon F, Yang A;
XX
DR WPI; 1999-277595/23.
DR N-PSDB; AAX58574.
XX
XX New isolated p63 cell regulatory protein for, e.g. treatment of
XX tumours
XX
XX Claim 23; Fig 11; 161pp; English.
XX
XX The present invention concerns the discovery of a new family of
XX cell regulatory proteins (CRPs) termed the p63 family of proteins,
XX which demonstrate certain sequence identity to known tumour
XX suppressor proteins p53 and p73. It has been observed that the
XX intron-exon organisation is conserved between p73 and p53, and from

```

CC known exon and intron sizes for these 2 genes, it was possible to
 CC identify new members of this gene family using a PCR-based strategy
 CC of amplifying 2 exons in a conserved domain and their intervening
 CC intron. The human p53 gene was localised to chromosomal position
 CC 3q27-29. At least 6 different isoforms exist. Splice variants
 CC differing at the C-terminus have been designated as alpha, beta and
 CC gamma forms, while p63 members differing in the N-terminus are
 CC designated as delta and TA forms, where the delta form lacks the
 CC transactivation domain. The present sequence represents human
 CC p63 isotype TAp63 gamma. p63 was detected in a variety of
 CC human and mouse tissue. It demonstrates remarkably divergent
 CC activities, such as the ability to transactivate p53 reporter genes
 CC and induce apoptosis. Cessation or down-regulation of p63 expression
 CC may play a critical role in the process of cervical squamous
 CC differentiation, both benign and neoplastic. DeltaN isoforms of p63
 CC act as dominant negatives towards transactivation by p53 and p63.
 CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
 CC cachexia) and neuronal differentiation and related degenerative
 CC disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see
 CC AAX3572-83) and anti-p63 antibodies of the invention can be used to
 CC identify compounds useful for treating disorders involving such
 CC processes, in detection and diagnosis, and in the production of
 CC transgenic animals.

XX Sequence 448 AA;

Query Match 9.3%; Score 186; DB 20; Length 448;
 Best Local Similarity 22.2%; Pred. No. 1e-10;
 Matches 75; Conservative 59; Mismatches 124; Indels 80; Gaps 15;

QY 5 QPMWHKSTEDSDST-EVDIKEDIPKTVYSGSELTTPMAFLQNSGMLQFSQQS 63
 Db 31 qpidinfvdepedgatnkiesmd---cirmqdsdl-sdpm-----wpdytulg 76

QY 64 VLEMMMLQDIQI---ANTLPKLENH-----NI 88
 Db 77 llnsm---dqqlngssstspyntdhaqsvtapsyaqpsstfdalspsaipsntdyp 133

QY 89 GGYCFSMVLDE---PPKSLMWSYIPLNKLIRNKAFFNVDVQFKSKMPQIPLNLRVFLCF 145
 Db 134 gphsfvdfqgsstaksatwtystelklyciaktcpig.kvmtppp-qgavirampvy 192

QY 146 --SNDVSAPVVRCONHLSVEPLTANNAKMRRESLLRSENPNVYCGNAQKGISE----RF 199
 Db 193 kkaehvtevrkrcpnahelsrefneggiappshlrve---gnshagyvedpitgrq 245

QY 200 SVVYPLNMSRSVTRSGLTROTTLAFKVFQNSCIG---RK: LVFCLERACGDIVGQHVI 256
 Db 246 svlvpy----epqvgteftvlynfmcnsccvggmrrj iivltletrdqvlgrrcf 301

QY 257 HVKICTCPKRDRIQDEROLNKKRKSVPFAAEDEPSK 294
 Db 302 earicacpgrdrkade---dsirkqgvdsdtkngdgtk 336

RESULT 14
 AAB11359
 ID AAB11359 standard; Protein; 448 AA.
 XX AAB11359;
 AC AAB11359;
 XX
 DT 21-FEB-2001 (first entry)
 XX
 DE Human p63 protein isoform #3.
 XX
 KW Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
 KW vaccine; detection.
 XX
 OS Homo sapiens.
 XX
 PN WO200061612-A2.
 XX

PD 19-OCT-2000.

XX 03-APR-2000; 2000WO-US08896.
 XX 02-APR-1999; 99US-0285479.
 PR 17-DEC-1999; 99US-0466396.
 PR 30-DEC-1999; 99US-0476496.
 PR 10-JAN-2000; 2000US-0480884.
 PR 22-FEB-2000; 2000US-0510376.
 XX (CORI-) CORIXA CORP.

XX Wang T, Fan L;
 XX WPI; 2000-628399/60.
 DR N-PSDB; AAC66029.

Isolated polypeptide comprising an immunogenic portion of a lung tumor protein is used for detecting and monitoring progression of lung cancer in a patient

XX Disclosure; Page 247-249; 261pp; English.

XX This invention describes a novel isolated polypeptide (I) which
 CC comprising an immunogenic portion of a lung tumor protein or variant (P2)
 CC which have cytostatic activity. The polypeptides and polynucleotides are
 CC used in compositions and vaccines to inhibit the development of cancer,
 CC especially lung cancer, in a patient. Methods described in the invention
 CC can be used to monitor the progression of a cancer by carrying out the
 CC detection at subsequent time points and comparing the results from the
 CC different time points. CD4+ and/or CD8+ T-Cells isolated from a patient
 CC are treated with P2, polynucleotides encoding P2 or antigen presenting
 CC cells expressing P2 and then administered to the patient to inhibit
 CC development of cancer.

XX Sequence 448 AA;

Query Match 9.3%; Score 186; DB 21; Length 448;
 Best Local Similarity 22.2%; Pred. No. 1e-10;
 Matches 75; Conservative 59; Mismatches 124; Indels 80; Gaps 15;

QY 5 QPMWHKSTEDSDST-EVDIKEDIPKTVYSGSELTTPMAFLQNSGMLQFSQQS 63
 Db 31 qpidinfvdepedgatnkiesmd---cirmqdsdl-sdpm-----wpdytulg 76

QY 64 VLEMMMLQDIQI---ANTLPKLENH-----NI 88
 Db 77 llnsm---dqqlngssstspyntdhaqsvtapsyaqpsstfdalspsaipsntdyp 133

QY 89 GGYCFSMVLDE---PPKSLMWSYIPLNKLIRNKAFFNVDVQFKSKMPQIPLNLRVFLCF 145
 Db 134 gphsfvdfqgsstaksatwtystelklyciaktcpig.kvmtppp-qgavirampvy 192

QY 146 --SNDVSAPVVRCONHLSVEPLTANNAKMRRESLLRSENPNVYCGNAQKGISE----RF 199
 Db 193 kkaehvtevrkrcpnahelsrefneggiappshlrve---gnshagyvedpitgrq 245

QY 200 SVVYPLNMSRSVTRSGLTROTTLAFKVFQNSCIG---RK: LVFCLERACGDIVGQHVI 256
 Db 246 svlvpy----epqvgteftvlynfmcnsccvggmrrj iivltletrdqvlgrrcf 301

QY 257 HVKICTCPKRDRIQDEROLNKKRKSVPFAAEDEPSK 294
 Db 302 earicacpgrdrkade---dsirkqgvdsdtkngdgtk 336

RESULT 15
 AAY05954
 ID AAY05954 standard; Protein; 516 AA.
 XX AAY05954;
 AC AAY05954;
 XX

DT 16-AUG-1999 (first entry)
 XX Human cell regulatory protein p63, isoform huTap63 beta.
 DE
 DE Cell regulatory protein; p63; huTap63 beta; Tap63 beta; human;
 KW cancer; tumour suppressor; cell cycle control; apoptosis;
 KW cell proliferation; cell differentiation; their py.
 XX
 OS Homo sapiens.
 XX
 XX W09919357-A2.
 PN
 XX 22-APR-1999.
 PD
 XX
 XX 02-OCT-1998; 98WO-US21992.
 PF
 XX 29-MAY-1998; 98US-0087216.
 PR
 XX 15-OCT-1997; 97US-0062076.
 XX
 XX (HARD) HARVARD COLLEGE.
 PA
 XX McKeon F, Yang A;
 PI
 XX WPI: 1999-277595/23.
 DR
 XX N-PSDB; AAX58573.
 XX
 XX New isolated p63 cell regulatory protein for, e.g. treatment of
 PT tumours
 PT
 XX
 XX Claim 23; Fig 10; 161pp; English.
 PS
 XX
 CC The present invention concerns the discovery of a new family of
 CC cell regulatory proteins (CRPs) termed the p63 family of proteins,
 CC which demonstrate certain sequence identity to known tumour
 CC suppressor proteins p53 and p73. It has been observed that the
 CC intron-exon organisation is conserved between p73 and p53, and from
 CC known exon and intron sizes for these 2 genes, it was possible to
 CC identify new members of this gene family using a PCR-based strategy
 CC of amplifying 2 exons in a conserved domain and their intervening
 CC intron. The human p53 gene was localised to chromosomal position
 CC 3q27-29. At least 6 different isoforms exist. Splice variants
 CC differing at the C-terminus have been designated as alpha, beta and
 CC gamma forms, while p63 members differing in the N-terminus are
 CC designated as deltaN and TA forms, where the deltaN form lacks the
 CC transactivation domain. The present sequence represents human
 CC p63 isoform Tap63 beta. p63 was detected in a variety of
 CC human and mouse tissue. It demonstrates remarkably divergent
 CC activities, such as the ability to transactivate p53 reporter genes
 CC and induce apoptosis. Cessation or down-regulation of p63 expression
 CC may play a critical role in the process of cervical squamous
 CC differentiation, both benign and neoplastic. DeltaN isoforms of p63
 CC act as dominant negatives towards transactivation by p53 and p63.
 CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
 CC cachexia) and neuronal differentiation and related degenerative
 CC disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see
 CC AAX58572-83) and anti-p63 antibodies of the invention can be used to
 CC identify compounds useful for treating disorders involving such
 CC processes, in detection and diagnosis, and in the production of
 CC transgenic animals.
 XX
 XX Sequence 516 AA;

Query Match 9.3%; Score 186; DB 20; Length 516;
 Best Local Similarity 22.2%; Pred. No. 1.3e-10;
 Matches 75; Conservative 59; Mismatches 124; Indels 80; Gaps 15;
 QY 5 QPMSWHKSTDESDST-EVDIKEDIPKTVESGSELTPENAFQLQGLNSNLWQFSQOS 63
 DB 31 qpIdlnfvdepsedgatnkielemd---cirmqsdsl-sdpm-----wpqytnlg 76
 QY 64 VLREMMIQQDIQIQ---ANTPLPLENH-----NI 88

Db 77 llnsm---dqiqngssstsyntdhagnsvtapsyagpsstfdalspsaipsntdyp 133
 QY 89 GGYCFSMVLDE---PPKSLWMYSIPLNKLIRMKAFNVDVQFKSKMPIOPLNRYFLCF 145
 Db 134 gphfdfsfgsstaksatwtystelklycqiaktcpidkivmtppp-ggavirampvy 192
 QY 146 --SNDVSAPYVRCQNHLSVEPLTANNKWRRESLRSNPNSVYCGNAOQKGISE-----RF 199
 Db 193 kkaehvtvkvrcpnhelsrefneggiappshllirve-----gnshaqyvedpitgrq 245
 QY 200 SVVYPLWMSRSVTRSGLTROTTLAFKVCQNSCIG---RKETSLVFCLEKACGDIVGQHV 256
 Db 246 svlvpy----epqvgvtefttvlvymonsscvggmmrrpilliivltetrdqvgvlgrrcf 301
 QY 257 HVKICTCPKRDRIQDERQLNSKKRKSVPPEAAEEDPSK 294
 Db 302 earicacpgrdrkade---dsirkqvsdstkngdgtk 336

Search completed: November 16, 2001, 15:49:07
 Job time: 2734 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2001, 15:05:43 ; Search time 31.25 Seconds
(without alignments)
277.241 Million cell updates/sec

Title: US-09-524-101-2

Perfect score: 2008
Sequence: 1 MYISQPMWHKSTEDSDS.....NLRHANKLSLKKRAYELP 385

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2.6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2.6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2.6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2.6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2.6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2.6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB	ID	Description
1	183.5	9.1	381	4	US-09-257-580-2	Sequence 2, Appli
2	167.5	8.3	390	1	US-08-347-792-15	Sequence 15, Appl
3	167.5	8.3	390	1	US-08-431-357-15	Sequence 15, Appl
4	167.5	8.3	390	4	US-08-392-542-3	Sequence 3, Appli
5	167.5	8.3	390	4	US-08-894-327-3	Sequence 3, Appli
6	167.5	8.3	390	5	PCT-US95-15353-15	Sequence 15, Appl
7	162	8.1	393	2	US-08-697-221-4	Sequence 3, Appli
8	162	8.1	393	2	US-08-697-221-4	Sequence 4, Appli
9	160	8.0	363	2	US-08-697-221-18	Sequence 18, Appl
10	160	8.0	393	1	US-08-047-041A-25	Sequence 25, Appl
11	160	8.0	393	1	US-08-047-041A-26	Sequence 26, Appl
12	160	8.0	393	1	US-08-047-041A-27	Sequence 27, Appl
13	160	8.0	393	1	US-08-047-041A-28	Sequence 28, Appl
14	160	8.0	393	1	US-08-347-792-2	Sequence 2, Appli
15	160	8.0	393	1	US-08-390-516C-6	Sequence 6, Appli
16	160	8.0	393	1	US-08-390-516C-7	Sequence 7, Appli
17	160	8.0	393	1	US-08-390-516C-8	Sequence 8, Appli
18	160	8.0	393	1	US-08-390-516C-9	Sequence 9, Appli
19	160	8.0	393	1	US-08-431-357-2	Sequence 2, Appli
20	160	8.0	393	1	US-08-390-515A-6	Sequence 6, Appli
21	160	8.0	393	1	US-08-390-515A-7	Sequence 7, Appli
22	160	8.0	393	1	US-08-390-515A-8	Sequence 8, Appli
23	160	8.0	393	1	US-08-390-515A-9	Sequence 9, Appli
24	160	8.0	393	2	US-08-795-006A-32	Sequence 32, Appl
25	160	8.0	393	2	US-08-697-221-2	Sequence 2, Appli
26	160	8.0	393	2	US-08-801-718-6	Sequence 6, Appli
27	160	8.0	393	2	US-08-801-718-7	Sequence 7, Appli

28 160 8.0 393 2 US-08-801-718-8 Sequence 8, Appli
29 160 8.0 393 2 US-08-801-718-9 Sequence 9, Appli
30 160 8.0 393 2 US-08-247-904B-12 Sequence 12, Appli
31 160 8.0 393 2 US-08-675-631-1 Sequence 1, Appli
32 160 8.0 393 3 US-08-767-942A-23 Sequence 2, Appli
33 160 8.0 393 4 US-08-392-542-2 Sequence 2, Appli
34 160 8.0 393 4 US-09-184-073-32 Sequence 32, Appli
35 160 8.0 393 4 US-08-328-673A-9 Sequence 9, Appli
36 160 8.0 393 4 US-08-894-327-2 Sequence 2, Appli
37 160 8.0 393 5 PCT-US95-15353-2 Sequence 2, Appli
38 160 8.0 439 2 US-08-959-638-9 Sequence 9, Appli
39 159 7.9 393 2 US-08-697-221-15 Sequence 15, Appli
40 158 7.9 363 2 US-08-697-221-17 Sequence 17, Appli
41 158 7.9 393 2 US-08-697-221-14 Sequence 14, Appli
42 158 7.9 393 2 US-08-697-221-27 Sequence 27, Appli
43 157 7.8 363 2 US-08-697-221-22 Sequence 22, Appli
44 157 7.8 393 2 US-08-697-221-12 Sequence 12, Appli
45 157 7.8 393 2 US-08-697-221-16 Sequence 16, Appli

ALIGNMENTS

RESULT 1
US-09-257-580-2
; Sequence 2, Application US/09257580
; Patent No. 6307036
; GENERAL INFORMATION:
; APPLICANT: Yorkshire Cancer Research
; TITLE OF INVENTION: Tumour Suppressor Gene
; FILE REFERENCE: Canine p53
; CURRENT APPLICATION NUMBER: US/09/257,580
; CURRENT FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: 9804178.3
; PRIOR FILING DATE: 1998-02-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Canis
; US-09-257-580-2

Query Match 9.1%; Score 183.5; DB 4; Length 381;
Best Local Similarity 23.3%; Pred. No. 2.4e-11;
Matches 66; Conservative 45; Mismatches 109; Indels 63; Gaps 11;
Qy 105 WMYSIPLNKLXIRKNAFNVDFKSKMPTQPLNLRVFLCF--SNDVSAVPVRCNHLNV 162
Db 111 WYSPLLNKLFCOLAKTCPQLWVSSPPPPNTC-VRAMAIYKKSEFVTVVRCPPHERC 169
Qy 163 EPTANNAMRESLLRSNPNSVYCGNAQKGISE-----RFSVVVPLMNSRVSRTSLTR 218
Db 170 SD-SSDGLAPPOHLIRVE-----GNLRKLYLDDRNTRFHSVVVPY----EPEVGSY 217
Qy 219 QTLAKFVQNSCIG---RKETSLVFCLEKAGDVGQHVHVXICTCPRDRIDQEROL 275
Db 218 TTHYNYMNSCGMGNRRPILITITLEDSSGNVLRNSFEVRVVCACPGDRRTEENF 277
Qy 276 NSKKRSVPAAAEDEFSKYRCAIAKTEDTSNDRCDSDAAEWNVSRTPDGYRLAI 335
Db 278 HKK-----GECPPFPFGSKRALPFTSTSSPPQKKPL-----DGEY----- 315
Qy 336 TPCNKELLQSTECMIKEAAAEVLRNPQENLRHANKLLSLK 378
Db 316 -----FTIQ-----IRGRERYEMFRNLNEALELK 339
RESULT 2
US-08-347-792-15
; Sequence 15, Application US/08347792
; Patent No. 5573925

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; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,357
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/347,792
; FILING DATE: 28-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST58USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9206
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 390 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-431-357-15

Query Match 8.38; Score 167.5; DB 1; Length 390;
Best Local Similarity 25.6%; Pred. No. 1.3e-09;
Matches 60; Conservative 38; Mismatches 95; Indels 41; Gaps

QY 107 YSIPLKLYIRMKAFNVDOFKSKPIQLPLNLRVLCF--SNDVSAPVVRQNHLSVEP 164
Db 123 YSPPLKILFQLVKYKCPQL--WVSATPPAGSRVRAAIYKKSQHTVEVVRCPHERCS- 180
QY 165 LTANNAKMRSLIRSENPSYCNAGQAGISE---RFSVYVPLNMSRVSRTSLRQT 220
Db 181 -DGDGLAPPHQLRVE-----GNLYPEYLEDRTQTFHSHVVVPY----EPEAGSEYTT 228
QY 221 LAFKVFQNCISG---RKETSILVFLCKKAGDVGQHVHVKICTCPKRDRIQDEROLNS 277
Db 229 IHKYMVCNBSGCMGMRRRPILTIITLSDSGNLLGRDSFEVRVCACPGDRRTTEENFR- 287
QY 278 KKRKSVPEARAEDESKVRRICIAKTEDIESNDSRDCDDSAEWNVSRTPGDGY 331
Db 288 KKEVLCPHEL-----PPGSAKRALPTCT-----SASPPQKKKLQGEY 324

RESULT 4
US-08-392-542-3
; Sequence 3, Application US/08392542
; Patent No. 6169073
; GENERAL INFORMATION:
; APPLICANT: Halazonetis, Thanos
; APPLICANT: Hartwig, Wolfgang
; TITLE OF INVENTION: Peptides and Peptidomimetics with
; TITLE OF INVENTION: Structural Similarity to Human p53 That Activate
; TITLE OF INVENTION: Function
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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Query Match 8.3%; Score 167.5; DB 4; Length 390;
Best Local Similarity 25.6%; Pred. No. 1.3e-09;
Matches 60; Conservative 38; Mismatches 95; Indels 41; Gaps 10;

Query Match	8.3%	Score 167.5;	DB 5;	Length 390;
Best Local Similarity	25.6%	Pred. No. 1.3e-09;		
Matches 60;	Conservative 38;	Mismatches 95;	Indels 41;	

[illegible]

RESULT

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; Sequence 4, Application US/08697221
;
; Patent No. 5847083
;
; GENERAL INFORMATION:
;
; APPLICANT: Halazonetis, Thanos D.
;
; TITLE OF INVENTION: Modified p53 Constructs and Uses
;
; NUMBER OF INVENTIONS: Therefor
;
; NUMBER OF SEQUENCES: 33
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: Howson and Howson
;
; STREET: Spring House Corporate Cntr., PO Box 457
;
; CITY: Spring House
;
; STATE: Pennsylvania
;
; COUNTRY: USA
;
; ZIP: 19477
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: i-tentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/697,221
;
; FILING DATE:
;
; CLASSIFICATION: 530
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: US 60/004,802
;
; FILING DATE: 22-SEP-1995
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: Kodroff, Cathy A.
;
; REGISTRATION NUMBER: 33,980
;
; REFERENCE/DOCKET NUMBER: WST64AUSA
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: 215-540-9206
;
; TELEFAX: 215-540-5818
;
; INFORMATION FOR SEQ ID NO: 4:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 393 amino acids
;
; TYPE: amino acid
;
; STRANDEDNESS:
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein
;
; US-08-697-221-4

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Query Match 8.1%; Score 162; DB 2; Length 393;
Best Local Similarity 23.0%; Pred. No. 5.3e-09;
Matches 65; Conservative 52; Mismatches 121; Indels 44; Gaps 11;

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Db 232 THYNMCSNGMGNRRPILITLEDSSGNLLGRNSFEVRVVCACPGDRRKRKEENLRK 291
QY 278 KKKSVPEAAEEDPSKVRRCIAIKTEDSNDSDCCDSSAAEWNVSRTPDGDYRLAITC 337
Db 292 K-----GEPHHELPGSTKRALPNT-----SSSQPKKKPLDGEYFTQIR 333
QY 337 CPNKEWLLQSTEGMIKEAAAEVLNPNQENLRHANKLLSLK 378
Db 334 GRERFENFRELNEALELKDAQAKEPG--GSAHSHSLKSKK 373

RESULT 9
US-08-697-221-18
; Sequence 18, Application US/08697221
; Patent No. 5847083
; GENERAL INFORMATION:
; APPLICANT: Halazonetis, Thanos D.
; TITLE OF INVENTION: Modified p53 Constructs and Uses
; TITLE OF INVENTION: Therefor
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr., PO Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/697,221
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/004,802
; FILING DATE: 22-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kodroff, Cathy A.
; REGISTRATION NUMBER: 33,980
; REFERENCE/DOCKET NUMBER: WST64AUSA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9206
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 363 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-697-221-18

Query Match 8.0%; Score 160; DB 2; Length 363;
Best Local Similarity 22.8%; Pred. No. 7.7e-09;
Matches 64; Conservative 47; Mismatches 106; Indels 64; Gaps 11;

QY 107 YSIPLNKLYIRMNKAFLNVDQFKSMPIQPLNLRVFLCF--SNDVSAPVVRQNHLSVEP 164
Db 126 YSPALNKAFLQAKTQVQLWVDSTPP--PGTVFRAMAIYKQSHQTEVVRCPHERCS- 183
QY 165 LTANNKMRSLRSENPNPNSVCGNAQKGISE-----RFSVVVPLNMSRVSRLTRQT 220
Db 184 -DSGLAPPQHLLRVE-----GNLRVEYLLDRNTRFHSVVVPY----EPPEVGSDDCT 231
QY 221 LAEFKVCQNSICG---RKETSIVFLCEKACGDIYGVQHVHVKICICPKRDRIDQERQLNS 277
Db 232 THYNMCSNGMGNRRPILITLEDSSGNLLGRNSFEVRVVCACPGDRRKRKEENLRK 291

QY 278 KKKSVPEAAEEDPSKVRRCIAIKTEDSNDSDCCDSSAAEWNVSRTPDGDYRLAITC 337
Db 292 K-----GEPHHELPGSTKRALPNT-----SSSQPKKKPLDGEY----- 327
QY 338 PNKEWLLQSTEGMIKEAAAEVLNPNQENLRHANKLLSLK 378
Db 328 ----FTLQ-----IRGRERFEMFRELNEALELK 351

RESULT 10
US-08-047-041A-25
; Sequence 25, Application US/08047041A
; Patent No. 5527676
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Baker, Suzanne J.
; APPLICANT: Fearon, Eric R.
; APPLICANT: Nigro, Janice M.
; TITLE OF INVENTION: Detection of Loss of the Wild-Type p53
; TITLE OF INVENTION: Gene
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001.4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/047,041A
; FILING DATE: 22-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/928,661
; FILING DATE: 17-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/446,584
; FILING DATE: 06-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/330,566
; FILING DATE: 29-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42917
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 393 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; AUTHORS: Buchman, et al.,
; JOURNAL: Gene
; VOLUME: 70
; PAGES: 245-252
; DATE: 1988
US-08-047-041A-25

Query Match 8.0%; Score 160; DB 1; Length 393;

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Best Local Similarity 23.0%; Pred. No. 8.8e-09;
Matches 65; Conservative 51; Mismatches 122; Indels 44; Gaps 11;

QY 107 YSIPLNKLYIRMNKAENVDVQKSKMPTQIPLNLRVFLCF--SNDYSADVVRCONHLSVPE 164
    || ||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 126 YSPALNMKMFQLAKTCPVOLWYDSTPP-PGTRVRAVAIYKQSOHTEVVRCPHHEKCS- 183
    :: ||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 165 LTANNKMRRESLIRSENPNISYCGNAQKGISE-----RFSVYVPLNMSRSVTRSGLTROT 220
    :: ||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 184 -DSOGLAPPQHILRVE-----GNLRVEYLDLRNTRFHSVVVPY----EPPEVGSDCVT 231
    :: ||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 221 LAFEFVQNSCIG---RKETSLVFLEKACGDIVGQHVHIVKICTCPKRRIDQEROLNS 277
    : : : : ||||: : : : : : : : : : : : : : : : : : : : : : : : :
Db 232 IHYMYNCSNCGMGRNRPILITLEDSSGNLLGRNSFEVRVCACPGQDRTEENLRK 291
    : : : : ||||: : : : : : : : : : : : : : : : : : : : : : : : :
QY 278 KKRKSVPEAAEEDPSKVRRCIAIKTETESNDSROCDSDAAEWNVSRTPDGY-RLAIT 336
    | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 292 K-----GEPHPELPQSTRALPNVT-----SSSPQPKKPLDGEYFTLIQR 333
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 337 CPNKEWLLQSIGMIKEAAAEVLRNPQENLRHANKLLSLK 378
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 334 GRERFEMFRELNEALELKDAQAGKEPG--GSRASHSHLSKK 373
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
US-08-047-041A-26
; Sequence 26, Application US/08047041A
; Patent No. 5527676
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Baker, Suzanne J.
; APPLICANT: Fearon, Eric R.
; APPLICANT: Nigro, Janice M.
; TITLE OF INVENTION: Detection of Loss of the Wild-Type p53
; TITLE OF INVENTION: Gene
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001.4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/047,041A
; FILING DATE: 22-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/928,661
; FILING DATE: 17-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/446,584
; FILING DATE: 06-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/330,566
; FILING DATE: 29-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42917
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 393 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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FILING DATE: 06-DEC-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/330,566
 FILING DATE: 29-MAR-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: Kagan, Sarah A.
 REGISTRATION NUMBER: 32,141
 REFERENCE/DOCKET NUMBER: 01107.42917
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-508-9100
 TELEFAX: 202-508-9299
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 393 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 PUBLICATION INFORMATION:
 AUTHORS: Harris, et al.,
 JOURNAL: Mol. Cell. Biol.
 VOLUME: 6
 ISSUE: 12
 PAGES: 4650-4656
 DATE: 1986
 US-08-047-041A-27

Query Match 8.0%; Score 160; DB 1; Length 393;
Best Local Similarity 23.0%; Pred. No. 8.8e-09;
Matches 65; Conservative 51; Mismatches 122; Under 44; Gaps 11;

QY	107	YSIPLNKLYIRNKAFAFNDVQVQFSKMPQIPLNLRFVFLCF---SNDVSAPVV_	QNHLSSVEP	164
Db	126	YSPALNKMCQIAKTCPCVLQWLDSTPP-PGTRVMAIYIKQSHMTVEYVRCPH	ERCS-183	
QY	165	LTANNAKMRESLLRGENPSVYCGNAGGISE---RFSVVPLNMSRSTRSGLTROT	220	
Db	184	-DSOGLAPQHLRVE-----GNLRVEYLDNRNTHFSVVVPY-----EP	EVGSDCTT	231
QY	221	LAFTVYQNSCTIG---RKETSLVFLCACKGDIQGVHIVKTCPTCKRDIODEROL	NS	277
Db	232	IHYWYMCNSCGMGNRRPILTIITLSDSGNLLGRNSFEYRVYCAPGURARTEEN	LRK	291
QY	278	KKRSVPEAAEEDPSKVRYRCIAIKTDETSNDRCDGSAAEWNVSRTPGDGY-	RLAIT	336
Db	292	K-----GEPHHELPGSTKRALPNNT-----SSPQPKKPLQGEYFTLQIR	333	
QY	337	CPNKWILLQSIEMGTEKAAAEVLNPNQENLRHANKLLSLK	378	
Db	334	GRETFEMFRELFALEKDAQACKEPG--GSRHSSHLKSKK	373	

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RESULT 13
US-08-047-041A-28
; Sequence 28, Application US/08047041A
; Patent No. 5527676
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Baker, Suzanne J.
; APPLICANT: Fearon, Eric R.
; APPLICANT: Niño, Janice M.
; TITLE OF INVENTION: Detection of Loss of the wild-type p53
; TITLE OF INVENTION: Gene
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: D.C.

```

```

RESULT 14
US-08-347-792-2
; Sequence 2, Application US/08347792
; Patent NO. 5573925
; GENERAL INFORMATION:
; APPLICANT: Halazonetis, Thanos D.
; TITLE OF INVENTION: p53 Proteins With Altered
; TITLE OF INVENTION: Tetramerization Domains
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr., PO Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/347,792
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST58USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9206
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 393 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-347-792-2

```

```

Query Match      8.0%; Score 160; DB 1; Length 393;
Best Local Similarity 23.0%; Pred. No. 8.8e-09;
Matches 65; Conservative 51; Mismatches 122; Indels 44; Gaps 11;

QY 107 YSIPLNKLYITMKKATFNVDVQFKSKMPTQPLNLRVFLCP--VDVSAPVPCQNHLSVEP 164
      || |||::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 126 YSPALNKMFCQLAKTQPCVQIOWDSTPP--PGTRVRAMATYKQ HMTVEVVRPCPHRCS- 183
      || |::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 165 LTANNAMKRESLRGNSPNVSYCGNAOCKGISE----RFSV PLNMRSYVTRSGLTRQT 220
      || |::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 184 -DSUGLAPPQHLIRVE-----GNLRVEYLDDNRTFRSHVAPY-----EPEVGSDCIT 231
      || |::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 221 LAFKVFQNSCGIG---RKETSIVFLCERACDVIQGVHVHVKICPCPKDRDIQDERLNS 277
      || |::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 232 IHYNWCMNSCGMKMRPILLIITLEDSSGNLLGRNSFEVRCVACPGDRDTEENLWK 291
      || |::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 278 KKRKSVPEAAEEDPCKVRRCAIKTEDTESNDRCDSDSAAEWNVSRTPDGDY-RLAIT 336
      || |::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 292 K-----GEPHHELPGSTKRALPNNT-----SSSQPKKKPLDGEYFTLIQR 333
      || |::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 337 CPNKEWLLQSGIEWKEAAAEVLRNPQENLRHANKLLSLK 378
      || |::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 334 GREKFEFMRNEALBKDAQAGKPG--GSRASHSLKSKK 373
      || |::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

RESULT 15
US-08-390-516C-6
; Sequence 6, Application US/08390516C
; Patent NO. 5708136
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARLEE
; APPLICANT: HILL, DAVID E.

```

1  APPLICANT: KINZLER, KENNETH W.
2  APPLICANT: VOGELSTEIN, BERT
3  TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
4  TITLE OF INVENTION: HUMAN TUMORS
5  NUMBER OF SEQUENCES: 9
6  CORRESPONDENCE ADDRESS:
7  ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
8  STREET: 1001 G STREET, N.W.
9  CITY: WASHINGTON
10 STATE: D.C.
11 COUNTRY: USA
12 ZIP: 20001
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Floppy disk
15 COMPUTER: IBM PC compatible
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 SOFTWARE: PatentIn release #1.0, Version #1.25
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/08/390,516C
20 FILING DATE: 07-APR-1993
21 CLASSIFICATION: 530
22 ATTORNEY/AGENT INFORMATION:
23 NAME: KAGAN, SARAH A.
24 REGISTRATION NUMBER: 32,141
25 REFERENCE/DOCKET NUMBER: 01107.42798
26 TELECOMMUNICATION INFORMATION:
27 TELEPHONE: 202-508-9100
28 TELEFAX: 202-508-9299
29 TELEX: 197430 BBMB UT
30 INFORMATION FOR SEQ ID NO: 6:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 393 amino acids
33 TYPE: amino acid
34 TOPOLOGY: linear
35 MOLECULE TYPE: protein
36 HYPOTHETICAL: YES
37 ANTI-SENSE: NO
38 ORIGINAL SOURCE:
39 ORGANISM: Homo sapiens
40 PUBLICATION INFORMATION:
41 AUTHORS: Buchman, et al.,
42 JOURNAL: Gene
43 VOLUME: 70
44 PAGES: 245-252
45 DATE: 1988
46 US-08-390-516C-6

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Query Match      8.0%; Score 160; DB 1; Length 393;
Best Local Similarity 23.0%; Pred. No. 8.e-09;
Matches 65; Conservative 51; Mismatches 122; Indels 44; Gaps 11;

QY 107 YSIPLNKLYIRMKAKFNVDVQPKSKMPTQPINLRVFLCF--SNDVSAPVPRQNHLSVPEP 164
    || |||::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 126 YSPALNKMFQCLAKTQVQLWLDSTPP--PGTRVRAMALYKQSOHMTVEVRRCPHHERCS- 183

QY 165 LFNANAKWRSLARSENPSVVCNGNAOCKGLISE----RFSVVVPLNMRSVTSRGLTROT 220
    ::::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 184 -DSGGLAPPQHLIRVE-----GNLRVEYLDORNTFRHSVVVPY----EPEVSGDCTT 231

QY 221 LAFKPVQNSCIG---RKETSLVFLCKKACDITVGQVHTVVKICTPKRDRIDDERQLNS 277
    ::::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 232 THYNYMCSNGMGNRRPILITLEDSSGNLLGRNSFEVRCACGDRDRTEENLRK 291

QY 278 KKRKSVPEAAEEDPSKVRRCIAKTEDTSNDRCDSDSAEAMWNSVSTPDGY--RLAIT 336
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 292 K-----GEPHHELPGSTKRALPNNT-----SSSPQPKKPLDGEYFFLQIR 333

QY 337 CPNKEWLLQSGIEMIKAAAEAVLRNPQOENLRHANKLLSLK 378

Db 334 GREFFEMFRELNEALBKDAQAGKEPG--GSRASHSHLKSKK 373

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Search completed: November 16, 2001, 15:49:51
Job time: 2648 sec

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	183	9.1	391	1	S02192	cellular tumor ant
2	180.5	9.0	386	1	S51648	cellular tumor ant
3	176.5	8.8	363	1	A23976	cellular tumor ant
4	174	8.7	396	1	S06333	cellular tumor ant
5	171	8.5	381	2	JH8824	cellular tumor ant
6	168.5	8.4	390	1	DNK553	cellular tumor ant
7	168	8.4	367	1	S02193	cellular tumor ant
8	168	8.4	393	2	JC6176	tumor suppressor p
9	165.5	8.2	391	2	JC6193	tumor suppressor p
10	164.5	8.2	396	1	JH0631	cellular tumor ant
11	160	8.0	393	1	DNH553	cellular tumor ant
12	152	7.6	393	1	S06594	cellular tumor ant
13	111	5.5	1036	2	V05687	beta-galactosidase
14	111	5.5	1852	1	VJC082	vitellogenin II pr
15	103.5	5.2	314	2	D96703	hypothetical prote
16	98.5	4.9	612	2	T15211	hypothetical prote
17	98.5	4.9	645	2	E96631	hypothetical prote
18	98.5	4.9	1181	2	T19736	probable receptor
19	97.5	4.9	1148	2	T13347	hypothetical prote
20	97.5	4.9	1475	2	T33318	Cnn protein - frui
21	96.5	4.8	507	2	T26530	hypothetical prote
22	96.5	4.8	646	2	T33346	hypothetical prote
23	96.5	4.8	1250	2	T22845	hypothetical prote
24	96	4.8	840	2	T21333	hypothetical prote
25	95.5	4.8	1137	2	T19414	hypothetical prote
26	95	4.7	1394	2	S60762	IgA-specific serin
27	95	4.7	1558	2	B71603	RTSA-H3 antigen Pf
28	94.5	4.7	697	2	B44489	GR box-binding pr
29	94	4.7	1244	2	T19068	hypothetical prote

Query Match	9.13;	Score 183;	DB 1;	Length 391;
Best Local Similarity	27.08;	Pred. No. 2.3e-07;		
Matches	58;	Conservative 36;	Mismatches 99;	Indels 22; Gaps 9;
QY	107	YSIPLANKLIIRNKAFFNDVQFKSKMFIQIPLNLRVPLCF--SNDVSPAPVYRCQNHLSVEP	164	
Ddb	124	YSISLNKLCFQIAKTCPQLWVTTPP--PQTRVRAMAIYKKSQHTEVVRCCPHHRCSS--	181	
QY	165	LTANNAKRESILLRSE--NPNSVYCGNAGKGISERFVVVPLNMSRVSRTSGITRGTFLAF	223	
Ddb	182	-DGDGLAPPQHLIRIVEGNPYAEYLDDRQ---TFRHSVVVPE---EPPEVGSDYTIHY	232	
QY	224	KFYVCONSGIG---RKETSIVPLEKAGDVIQGVHVIKICTPKCRDRIODERQLNSKKR	280	
Ddb	233	KYCNSSCGMGNRRPIITITLSDSSGNLLGRDGFVRCVACPGDRTEENFR--KKE	291	
QY	281	KSVPEAAEEDPSKVRRCIAIKTEDTSDNSRDCD	315	
Ddb	292	EHCPCL-----PPGSAKRALPTSTSSPOOKKKPLD	322	


```

A:Reference number: S72313
A:Accession: T72313
A:Molecule type: mRNA
A:Residues: 1-51, 'S', 53-70, 72-293, 295-363 <ROW>
A:Cross-references: EMBL:X77546; NID:g468513; PIDN:CAA54672.1; PID:g468514
C:Genetics:
A:Gene: p53
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; pho
F:150,153,213,217/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:362/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

      8.8%;   Score 176.5;  DB 1;   Length 363;
Best Local Similarity   26.2%;   Pred. No. 7e-07;
Matches 73;  Conservative 46;  Mismatches 119;  Indels 41;  Gaps 13;

QY  55  NLMQFSQOSVLREMLQDIIQIANTLPKLENNHI-----GGYCFSNVLDE--PKPSI- 104
      ||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db  38  NLSEPPDYPLAADMVTLQGLMGNAVPFVSCAVPTDDYAGKYLQIDFQQNGTKAKVT 97
      ||  |||||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY  105  WMYSIPLNKLYIRNKAFNVVDQFSKMPIQPLNLRVFLCF--SNDYSAPVVRQNH-LS 161
      ||  |||||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db  98  CTYSEPLNKLFCOLAKTCLPLLRVSPSPRGSI-LRATAVYKKSEHAEVVKRCPHHRS 156
      ||  |||||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY  162  VEPLTANNAKMRESLLSENPNVYCGNAQKGI----SERFVVVPLNMSRVTSGJLT 217
      |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db  157  VEP--GEDAAPPHLMRVE-----GNLQAYTMDVNSGRHSCVVPY----EGPVGTE 203
      ||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY  218  ROTLAFKVFQNSICG---RKETSILVPLEKACGDIVGQHVTHVKIKTCFKPRKDIDERQ 274
      ||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db  204  CTTVLYNVMCNSCGMMNRNPILLTIETPTQGLLLGRRCFEFVRCACGRDR-RTEED 262
      ||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY  275  LNSKRRKSVPEAAEE-----DEPSKVRRCIAIKTDETE 307
      :|||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db  263  NTKKRLKSGRELAHPSPPEPLPKPKRLVWVDDDEE 301
      :|||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

```

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RESULT      4
JH0633
cellular tumor antigen p53 - golden hamster
N:Alternate names: tumor-suppressor protein p53
C:Species: Mesocricetus auratus (golden hamster)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
R:Accession: JH0633
R;Legros, Y.; McIntyre, P.; Soussi, T.
Gene 112, 247-250, 1992
A>Title: The cDNA cloning and immunological characterization of hamster p53.
A:Reference number: JH0633; MUID:92210007
A:Accession: JH0633
A:Molecule type: mRNA
A:Residues: 1-396 <LEG>
A:Cross-references: GB:M75144; NID:g191415
A:Experimental source: kidney, strain MP1
C:Genetics:
A:Gene: p53
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; pho
F:179,182,241,245/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match          8.7%; Score 174; DB 1; Length 396;
Best Local Similarity 24.9%; Pred. No. 1.3e-06;
Matches 70; Conservative 51; Mismatches 118; Indels 42; Gaps 12;

QY   107 YSIPLNKLYITRMNKAFNVVDVGFKSMP-----IQPLNLRVFLCFSDNSAPVVRCONHLVS 162
    ||| |||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db   129 YSPSLNKLFCQLAKTCPVLWSSTPPGPRIVRAIMAYKKLQYMTVE---VRCRPH--E 183

QY   163 EPLTANNAKWRSELRLSE-NPNSVYTCGNAGKGIGERFSVVVPPLNMRSVTRSGLTROTLL 221
    : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db   184 RSSEGDGLAPPQHLLRVGGNNHAELDDQK----TFRHSSVVPVY---EPPEVGSDCTTI 235

```

Db 229 IHYKYNSSCGMNRRLPILITLEDSSNLGRDSFVRVCACPGDRRTTEENFR - 287

QY 278 KKRKSVPAEAEDEPSKVRRCIAKTKETESNDSDCCDSAAEWNYSRTDGPQDYRLAITC 337

Db 288 KKEVLCPDEL-----PPGSAKRALPTCT-----SASPQKKKPLDGEYFTLKIR 330

QY 338 PNKEW-----LLASIEGMIKEAAAEVLNRPNQENLRHANKLSLKKRAYE 383

Db 331 GRKRFEMFREINALE--LKDAHA-----TEESGDGRAHS-----SLOPRAFQ 371

RESULT 6

DNMS53

cellular tumor antigen p53 - mouse

N:Alternate names: oncoprotein p53

C:Species: Mus musculus (house mouse)

C:Date: 28-Aug-1985 #sequence_revision 04-Oct-1996 #text_change 11-May-2000

C:Accession: A22739; S06336; A02684; S38822; S38823; S40014; I48703

R:Bienz, B.; Zakut-Houri, R.; Givoli, D.; Oren, M.

EMBO J. 3, 2179-2183, 1984

A:Title: Analysis of the gene coding for the murine cellular tumour antigen p53.

A:Reference number: A22739; MUID:85027173

A:Accession: A22739

A:Molecule type: DNA

A:Residues: 1-134, 'V', 136-390 <BIE>

A:Cross-references: GB:X00876; NID:9871420; PIDN:CAA25420.1; PID:g871421; GB:X01237; R:Chumakov, P.M.

Bioorg. Khim. 13, 1691-1694, 1987

A:Title: Primary structure of DNA complementary to murine oncoprotein p53 mRNA.

A:Reference number: S06336; MUID:88221682

A:Accession: S06336

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-134, 'V', 136-390 <CHU>

R:Zakut-Houri, R.; Oren, M.; Bienz, B.; Lavie, V.; Hazum, S.; Givoli, D.

Nature 306, 594-597, 1983

A:Title: A single gene and a pseudogene for the cellular tumour antigen p53.

A:Reference number: A02684; MUID:84068204

A:Accession: A02684

A:Molecule type: mRNA

A:Residues: 1-159, 'H', 161-167, 'G', 169-233, 'I', 235-390 <ZAK>

A:Cross-references: GB:X01233; GB:X01700; NID:g53575

R:Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.

Mol. Cell. Biol. 6, 3232-3239, 1986

A:Title: Immunologically distinct p53 molecules generated by alternative splicing.

A:Reference number: S38822; MUID:87064640

A:Accession: S38822

A:Molecule type: mRNA

A:Residues: 1-390 <ARAI>

A:Cross-references: EMBL:M13872; NID:g200198; PIDN:AAA39881.1; PID:g200199

A:Accession: S38823

A:Molecule type: mRNA

A:Residues: 1-167, 'G', 169-233, 'I', 235-390 <ARA2>

A:Cross-references: EMBL:M13873

R:Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.

submitted to the EMBL data Library, July 1988

A:Reference number: S40014

A:Accession: S40014

A:Molecule type: mRNA

A:Residues: 1-167, 'G', 169-390 <ARA3>

A:Cross-references: EMBL:M13873; NID:g200200; PIDN:AAA39882.1; PID:g200201

R:Jeukens, J.R.; Rudge, K.; Redmond, S.; Wade-Evans, A.

Nucleic Acids Res. 12, 5609-5626, 1984

A:Title: Cloning and expression analysis of full length mouse cDNA sequences encoding

A:Reference number: I48703; MUID:84272240

A:Accession: I48703

A:Status: translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-47, 'R', 49-78, 'QW', 82-390 <RES>

A:Cross-references: EMBL:X00741; NID:g353570; PIDN:CAA25323.1; PID:g53571

C:Comment: This DNA-binding protein plays an essential role in the regulation of cell

C:Comment: The tetramer association region may exhibit a beta-turn, beta-sheet, beta-

C:Superfamily: cellular tumour antigen p53

C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; phosphoprotein;
F:1-44/Domain: transcription activation #status predicted <TRA>
F:16-26/Domain: conserved region I
F:199-289/Domain: DNA-binding core #status predicted
F:108-121/Region: L1 loop
F:114-139/Region: conserved region II
F:160-192/Region: L2 loop
F:168-178/Region: conserved region III
F:231-252/Region: conserved region IV
F:233-248/Region: L3 loop
F:267-283/Region: conserved region V
F:313-319/Region: nuclear location signal
F:319-357/Region: tetramer association
F:7-9,12,18,23,37/Binding site: phosphate (Ser) (covalent) #status predicted
F:173,176,235,239/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted
F:389/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 8.4%; Score 168.5; DB 1; Length 390;
Best Local Similarity 25.6%; Pred. No. 3.5e-06;
Matches 60; Conservative 38; Mismatches 95; Indels 41; Gaps 10;
QY 107 YSIPLNKLYIRMKAFNVDVQFKSMPIQPLNLRVFLCF--SNDVSAPVVRCONHLSVEP 164
DB 123 YSPLNKLFCQLAKTCPVQL-WVSATPPAGSRVRAMAIYKKSQHEVVRCPHHERCS- 180
QY 165 LTANNKMRRESLLRSNPNSVYCGNAGKGISB----RFSVVVPLNMSRVSRTSGTROT 220
DB 181 -DGDGLAPQHLIRVE-----GNLYPELDRQTFRHSVVVPY----EPPEAGSEYIT 228
QY 221 LAKFVQNSCIG--RKETSLVFLCKACGDIVGQHVHVKICTCPKRDRIQDERQLNS 277
DB 229 IHKYWCNCSGGMNRRPILITITLEDPSGNLLGRDSEVRVACPCGRDRTEENFR- 287
QY 278 KRKSVPEAAEEDPSKVRRCIAIKTDTESNDRDCDDSAAEWNVSRTPDGDY 331
DB 288 KKEVLPCL-----PPGSAKRALPCT-----SASPQKKPLDGEF 324

RESULT 7
S02193
cellular tumor antigen p53 - chicken
N:Alternate names: nuclear oncoprotein p53
C:Species: Gallus gallus (chicken)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S02193
R:Soussi, T.; Beque, A.; Kress, M.; Stehelin, D.; May, P.
Nucleic Acids Res. 16, 11383, 1988
A:Title: Nucleotide sequence of a cDNA encoding the chicken p53 nuclear oncoprotein.
A:Reference number: S02193; MUID:89083584
A:Accession: S02193
A:Molecule type: mRNA
A:Residues: 1-367 <SO>
A:Cross-references: EMBL:X13057; NID:g63740; PIDN:CAA31456.1; PID:g63741
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phospho
F:161,164,224,228/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:366/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 8.4%; Score 168; DB 1; Length 367;
Best Local Similarity 29.4%; Pred. No. 3.6e-06;
Matches 60; Conservative 29; Mismatches 89; Indels 26; Gaps 8;
QY 107 YSIPLNKLYIRMKAFNVDVQFKSMPIQPLNLRVFLCF--SNDVSAPVVRCONHLSVEP 164
DB 111 YSPVANKVYCLAKCPQVHRV-GVAPPGSSLRVAVYKSEHVAEVRRCPPHHERCGG 169
QY 165 LTANNKMRRESLLRSNPNSVYCGNAGKGISBFSVVVPLNMSRVSRTSGTROTIAFK 224
DB 170 GTDGLAPQHLIRVEGNPQARYHDEETK-----RHSVVVPY----EPPEVGSCTTVLYN 221

QY 225 FVQNSCIG---RKETSLVFLCKACGDIVGQHVHVKICTCPKRDRIQDERQLNSKKR 280
DB 222 FWCNSGCMGGMNRRPILITITLEDPSGQLLGRRCFVVRVACPCGRDRKITEE---NFRKR 278
QY 281 -----KSVPEAAEEDPSKVR 296
DB 279 GGAGVAKRAMSPPTAPEPPKKR 302
RESULT 8
JC6176
tumor suppressor protein p53 - Chinese hamster
C:Species: Cricetus griseus (Chinese hamster)
C>Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 23-Jul-1999
C:Accession: JC6176
R:Lee, H.; Larner, J.M.; Hamlin, J.L.
Gene 184, 177-183, 1997
A:Title: Cloning and characterization of Chinese hamster p53 cDNA.
A:Reference number: JC6176; MUID:97183659
A:Contents: liver
A:Accession: JC6176
A:Molecule type: mRNA
A:Residues: 1-393 <LEE>
A:Cross-references: GB:U50395; NID:g1842229; PIDN:AAC53040.1; PID:g1842230
C:Comment: This protein is a multimer, it plays the central role in a complex DNA dam
ption, and recombination by protein/protein interactions.
C:Genetics:
A:Gene: p53
C:Superfamily: cellular tumor antigen p53
C:Keywords: liver; tumor

Query Match 8.4%; Score 168; DB 2; Length 393;
Best Local Similarity 25.4%; Pred. No. 3.9e-06;
Matches 72; Conservative 52; Mismatches 113; Indels 46; Gaps 14;
QY 107 YSIPLNKLYIRMKAFNVDVQFKSMPIQPLNLRVFLCF--SNDVSAPVVRCONHLSV 162
DB 126 YPSLNLKFCQLAKTCPVQLWVNSTPPGTRVRAMAIYKKLQYMTFV---VRCPHH--E 180
QY 163 EPLTANNKMRRESLLRSE--NPNSVYCGNAGKGISERFSVVVPLNMSRVSRTSGLTRQTL 221
DB 181 RSSEGDLSAPPQHLIRVEGNLHAEYLDQK----TFRHSVVVPY----EPPEVGSCTCTI 232
QY 222 AFKVCQNSCIG---RKETSLVFLCKACGDIVGQHVHVKICTCPKRDRIQDERQLNSK 278
DB 233 HYNVCNCSGCMGGMNRRPILITITLEDPSGNLLGRNSFEVRCACPCGRDRTEENKF-QK 291
QY 279 KRKSVPEAAEEDPSKVRRCIAIKTDTESNDRDCDDSAAEWNVSRTPDGDY-RLAITC 337
DB 292 KGEPCPEL-----PPKSAKRALPTN-----SSSPPKKTLIDGEYFLAIRG 334
QY 338 PNKEWILQSI-EGM-IKEAAAEVLNPNQENLRHANKLLSLK 378
DB 335 HERKMPQELNEALELKDAQA-----SKGSDNGAHSSYLKSKK 373

RESULT 9
JC6193
tumor suppressor p53 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000
C:Accession: JC6193
R:Le Goas, F.; May, P.; Ronco, P.; de Fromental, C.C.
Gene 185, 169-173, 1997
A:Title: cDNA cloning and immunological characterization of rabbit p53.
A:Reference number: JC6193; MUID:97208869
A:Accession: JC6193
A:Molecule type: mRNA
A:Residues: 1-391 <LEA>
A:Cross-references: EMBL:X90592; NID:g1532043; PIDN:CAA62216.1; PID:g1532044
C:Genetics:
A:Gene: p53

QY 260 ICTCPKRDRIQDERQLNSKKRKSVPAAEEDPSKVRRCI 299
: | | | | : | : | | : : : :
: | | | | : | : | | : : : :

A:Cross-references: EMBL:X60019; NID:g506450; PIDN:CAA42634.1; PID:g506451
A:Accession: I38092
A>Status: translated from GB/EMBL/DDBJ
A>Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-253,'D','V',255-393 <F1>
A:MoleRule type: mRNA
A:Cross-references: EMBL:X60020; NID:g506452; PIDN:CAA42635.1; PID:g506453
A>Note: all sequences submitted to the EMBL/GenBank/DDJB databases June 1991
R:Futreal, P.A.; Barrett, J.C.; Wiseman, R.W.
Nucleic Acids Res. 19, 6977, 1991
A>Title: An Alu polymorphism intragenic to the TP53 gene.
A:Reference number: I38093; MOID:92107726
A:Accession: I38093
A>Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-393 <FUT>
A:MoleRule type: DNA
A:Cross-references: EMBL:X54156; NID:g35213; PIDN:CAA38095.1; PID:g35214
R:Yamada, Y.; Yoshida, T.; Havashi, K.; Sekiya, T.; Yokota, J.; Hirohashi, S.; Nakata
Cancer Res. 51, 5800-5805, 1991
A>Title: p53 gene mutations in gastric cancer metastases and in gastric cancer cell l
A:Reference number: A44905; MOID:92034678
A:Accession: A44905
A:Molecule type: DNA
A:Residues: 246-247,'W',249-250 <YAM>
A:Cross-references: GB:S63157; NID:g237829; PIDN:AAB20140.1; PID:g237830
A>Note: sequence extracted from NCBI backbone (NCBIN:63157, NCBP:63158)
A>Note: mutation from a liver metastasis of a gastric cancer
R:Hensel, C.H.; Xiang, R.H.; Sakaguchi, A.Y.; Naylor, S.L.
Oncogene 6, 1067-1071, 1991
A>Title: Use of the single strand conformation polymorphism technique and PCR to dete
A:Reference number: I58354; MOID:91296386
A:Accession: I58354
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 244-247,'W',249-252 <HEN1>
A:Cross-references: B:S41969; NID:g1679931; PIDN:AAB19324.1; PID:g232814
A:Accession: I78850
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 274-277,'S',279-282 <HEN2>
A:Cross-references: GB:S41977; NID:g1679932; PIDN:AAB19325.1; PID:g232816
R:Chow, V.T.; Quek, H.H.; Tock, E.P.C.
Cancer Lett. 73, 141-148, 1993
A>Title: Alternative splicing of the p53 tumor suppressor gene in the Molt-4 T-lympho
A:Reference number: I52681; MOID:94036762
A:Accession: I52681
A>Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 327-331,'DQTSFOKENC' <CHO>
A:Cross-references: GB:S66666; NID:g436292; PIDN:AAB28601.1; PID:g436293
A>Note: mutant sequence with altered splicing and termination expressed in Molt-4 T-1
R:Petersen, G.; Song, D.; Huegler-Doerr, B.; Oldenburg, I.; Bautz, E.K.F.
Mol. Gen. Genet. 249, 425-431, 1995
A>Title: Mapping of linear epitopes recognized by monoclonal antibodies with gene fra
A:Reference number: S60151; MOID:96133682
A:Accession: S60153
A:Molecule type: DNA
A:Residues: 3-44 <PET>
R:Dang, C.V.; Lee, W.M.F.
J. Biol. Chem. 264, 18019-18023, 1989
A>Title: Nuclear and nucleolar targeting sequences of c-erb-A, c-myc, N-myc, p53, HSP

Query Match 8.0%; Score 160; DB 1; Length 393;
Best Local Similarity 23.0%; Pred.No.1.8e-05;
Matches 65; Conservative 51; Mismatches 122; Indels 44; Gaps 11;

Qy 107 YSIPLNKLYIRMKAFNVDDYQFKSMPTQLNLRVLCF--SNDSAPVVRQCNHLSVEP 164
|| |||:::||||:::||||:::||||:::||||:::||||:::
Db 126 YSPALNNKFCQATCPVLWDSTFP-PGTRVMAAIYKQSHMTVEVRCPPHERCS- 183
:::||||:::||||:::||||:::||||:::||||:::
Qy 165 LTANNAKKRESLLRSNPNSVCYGNAQKGISE-----RFSVVVPLNMRSVSRLGLTR 220
:::||||:::||||:::||||:::||||:::||||:::
Db 184 -DSDDLGPQHLIRVE-----GNLRVEYLDDNRFRHSVVVPY----EPPEVGSDCTT 231

A:Map position: 4
A:Introns: 20/2; 118/2; 171/3; 251/2; 286/3; 315/1; 354/3; 410/3; 469/2; 506/1; 542/3;
A>Note: F20M13.150
C:Superfamily: beta-galactosidase bga

Query Match 5.5%; Score 111; DB 2; Length 1036;
Best Local Similarity 21.8%; Pred. No. 0.68;
Matches 71; Conservative 53; Mismatches 116; Indels 86; Gaps 16;

QY 5 QPMSWHKESTDESDTVDIEDIPKTVFVSSELTTPMAFLQGLNSGMLMQFSQQSV 64
Db :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
607 KPLTKYKYTFETPGVNAIVR-----MKAMKGKL-----IWNIGVGGRYW-MSLFLSP 654
QY 65 LREMMLODIQOANTLPKLENNHNGGYCFSMVLDEPPKSLWYSIP---LNKLYIRNKA 121
Db ||:||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
655 LGEPQTQTEHYHPRSFMKGEKKNM-----LVILEEPP-GVKLESIDFVLVNROTICSNVG 708
Db ||:||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
QY 122 FNVDVOFKS-----KMPIQLNLRLVLCFCSNDVASPVVRQC�HLSVEPLTANNAKNRES 175
Db ||:||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
709 EDYPVSVAWSMKREGPKIVSRKMDRL-----KAVMRC-----PPEKQMWEV 749
QY 176 LLRSNPNSVVCGN-AQGKGISERSFVVVPLNMSRVTSRSGLTROTTLAFKVFQNCSICGR 234
Db :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
750 QPASFGDPTGTCCGNFTMGK-----CSASKS-----KEVKEKECLGR 785
QY 235 KETSLSVFCLE-----KAGDIDVGQHVIHVKICTCPKDRIDOTERQOLNSKKRKSYPEAAEED 290
Db ||:||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
786 NCVSIIVARETFDGKGPVLVYTLAVQVK---CEKKEGQDEK----KKDEDKDEEEED 838
QY 291 EFSKYRRCAIAIKTEDTESNDSRDCCD 316
Db ||:||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
839 EDDDEE-----EEDKENKDTKDMEN 860

RESULT 14
VUCH2
vitellogenin II precursor [validated] - chicken
N:Contains: 40K yolk glycoprotein; lipovitellin; phosvitin
C:Species: Gallus gallus (Chicken)
C>Date: 28-Aug-1985 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C:Accession: I50441; S55680; A92941; A93502; C29184; I50440; S07788; E23876; A03335;
R:Nargelli, D.; van het Schip, F.D.; Gerber-Huber, S.; Haefliger, J.
J. Biol. Chem. 262, 15377-15385, 1987
A>Title: Comparison of the organization and fine structure of a chicken and a Xenopus
A:Reference number: I50441; MUID:88058863
A:Accession: I50441
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1852 <NAR>
A:Cross-references: GB:M18060; NID:g212880; PIDN:AAA49139.1; PID:g212881
R:Yamanura, J.; Adachi, T.; Aoki, N.; Nakajima, H.; Nakamura, R.; Matsuda, T.
Biochim. Biophys. Acta 1244, 384-394, 1995
A>Title: Precursor-product relationship between chicken vitellogenin and the yolk pro-

A:Reference number: S55680; MUID:95322425
A:Accession: S55680
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1569-1582 <YAMS>
R:van het Schip, F.D.; Samallo, J.; Broos, J.; Ophuys, J.; Mojet, M.; Gruber, M.; AB,
J. Mol. Biol. 196, 245-260, 1987
A>Title: Nucleotide sequence of a chicken vitellogenin gene and derived amino acid se
A:Reference number: A92941; MUID:88011328
A:Accession: A92941
A:Molecule type: DNA
A:Residues: 1-579,583-774,'R',776-1138,'S','1140-1437,'HK',1440-1852 <VAN>
A:Cross-references: GB:X13607; NID:g63886; PIDN:CAA31942.1; PID:g63887
A>Note: 1842-Ala was also found
R:Burch, J.B.E.
Nucleic Acids Res. 12, 1117-1135, 1984
A>Title: Identification and sequence analysis of the 5' end of the major chicken vite
A:Reference number: A93502; MUID:84118805
A:Accession: A93502
A>Note: 1842-Ala was also found

A:Accession: A93502
A:Molecule type: DNA
A:Residues: 1-71 <BUR>
A:Cross-references: GB:X00345; NID:963872; PIDN:CAA25096.1; PID:963873
R:Clark, R.C.
Int. J. Biochem. 17, 983-988, 1985
A:Title: The primary structure of avian phosvitins. Contributions through the Edman degradation
A:Reference number: A91754; MUID:86056531
A:Accession: C29184
A:Molecule type: protein
A:Residues: 1114-1138, 'S', 1140-1190 <CIA>
R:Byrne, B.M.; van Het Schip, A.D.; van de Klundert, J.A.
Biochemistry 23, 4273-4279, 1984
A:Title: Amino acid sequence of phosvitin derived from the nucleotide sequence of part of the chicken vitellogenin gene
A:Reference number: 150440; MUID:85023316
A:Accession: I50440
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1094-1138, 'S', 1140-1340 <BYR>
A:Cross-references: GB:X02113; NID:g212878; PIDN:AAA98791.1; PID:g212879
R:Phillipsen, J.N.J.; de Vries, J.E.; Samalio, J.; van Dijk, C.; Arnberg, A.C.; AB, G.
J. Mol. Evol. 28, 185-190, 1989
A:Title: Characterization of a polymorphism in the 3' part of the chicken vitellogenin gene
A:Reference number: S07788; MUID:89178745
A:Accession: S07788
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1707-1759 <ABG>
A:Cross-references: EMBL:X14729; NID:g63881; PIDN:CAA32851.1; PID:g1334751
A:Note: the source is designated as Gallus domesticus
R:Walker, P.; Brown-Luedi, M.; Germond, J.E.; Mahli, W.; Meijlink, F.C.P.W.; van het Schip, J. 2, 2271-2279, 1983
EMBO J. 2, 2271-2279, 1983
A:Title: Sequence homologies within the 5' end region of the estrogen-controlled d vitellogenin gene
A:Reference number: A23876; MUID:84131940
A:Accession: E23876
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-71 <WAL>
C:Comment: Vitellogenin is synthesized in the liver of oviparous vertebrates in response to estradiol
C:Comment: Phosvitin, an egg yolk storage protein, is one of the most highly phosphorylated proteins in the egg
C:Genetics:
A:Gene: VtgII
A:Introns: 14/1; 21/1; 71/3; 155/3; 209/3; 259/2; 309/3; 362/2; 417/3; 459/3; 532/3; 607/2; 1535/3; 1581/1; 1643/2; 1674/1; 1706/3; 1760/1; 1814/1
C:Superfamily: vitellogenin
C:Keywords: egg yolk; glycoprotein; liver; phosphoprotein
F:1-15/Domain: signal sequence #status predicted <SIG>
F:1114-1330/Product: phosvitin B #status experimental <MPT>
F:1125,1126,1127,1128,1129,1130,1132,1133,1137,1138,1140,1141,1142,1144,1145,1169,1170,1171,1192,1195,1196,1197,1198,1199,1200,1201,1202,1203,1204,1205,1206,1208,1209,1210,1211,1212,1213,1214,1242,1244,1245,1246,1247,1248,1249,1250,1251,1252,1253,1254,1256,1257,1258,1259,1260,1261,1262,1263,1264,1265,1266,1267,1268,1269,1270,1271,1272,1273,1274,1275,1276,1277,1278,1279,1280,1281,1282,1283,1284,1285,1286,1287,1288,1289,1290,1291,1292,1293,1294,1295,1296,1297,1298,1299,1300,1301,1302,1303,1304,1305,1306,1307,1308,1309,1310,1311,1312,1313,1314,1315,1316,1317,1318,1319,1320,1321,1322,1323,1324,1325,1326,1327,1328,1329,1330,1331,1332,1333,1334,1335,1336,1337,1338,1339,1340,1341,1342,1343,1344,1345,1346,1347,1348,1349,1350,1351,1352,1353,1354,1355,1356,1357,1358,1359,1360,1361,1362,1363,1364,1365,1366,1367,1368,1369,1370,1371,1372,1373,1374,1375,1376,1377,1378,1379,1380,1381,1382,1383,1384,1385,1386,1387,1388,1389,1390,1391,1392,1393,1394,1395,1396,1397,1398,1399,1400,1401,1402,1403,1404,1405,1406,1407,1408,1409,1410,1411,1412,1413,1414,1415,1416,1417,1418,1419,1420,1421,1422,1423,1424,1425,1426,1427,1428,1429,1430,1431,1432,1433,1434,1435,1436,1437,1438,1439,1440,1441,1442,1443,1444,1445,1446,1447,1448,1449,1450,1451,1452,1453,1454,1455,1456,1457,1458,1459,1460,1461,1462,1463,1464,1465,1466,1467,1468,1469,1470,1471,1472,1473,1474,1475,1476,1477,1478,1479,1480,1481,1482,1483,1484,1485,1486,1487,1488,1489,1490,1491,1492,1493,1494,1495,1496,1497,1498,1499,1500,1501,1502,1503,1504,1505,1506,1507,1508,1509,1510,1511,1512,1513,1514,1515,1516,1517,1518,1519,1520,1521,1522,1523,1524,1525,1526,1527,1528,1529,1530,1531,1532,1533,1534,1535,1536,1537,1538,1539,1540,1541,1542,1543,1544,1545,1546,1547,1548,1549,1550,1551,1552,1553,1554,1555,1556,1557,1558,1559,1560,1561,1562,1563,1564,1565,1566,1567,1568,1569,1570,1571,1572,1573,1574,1575,1576,1577,1578,1579,1580,1581,1582,1583,1584,1585,1586,1587,1588,1589,1590,1591,1592,1593,1594,1595,1596,1597,1598,1599,1600,1601,1602,1603,1604,1605,1606,1607,1608,1609,1610,1611,1612,1613,1614,1615,1616,1617,1618,1619,1620,1621,1622,1623,1624,1625,1626,1627,1628,1629,1630,1631,1632,1633,1634,1635,1636,1637,1638,1639,1640,1641,1642,1643,1644,1645,1646,1647,1648,1649,1650,1651,1652,1653,1654,1655,1656,1657,1658,1659,1660,1661,1662,1663,1664,1665,1666,1667,1668,1669,1670,1671,1672,1673,1674,1675,1676,1677,1678,1679,1680,1681,1682,1683,1684,1685,1686,1687,1688,1689,1690,1691,1692,1693,1694,1695,1696,1697,1698,1699,1700,1701,1702,1703,1704,1705,1706,1707,1708,1709,1710,1711,1712,1713,1714,1715,1716,1717,1718,1719,1720,1721,1722,1723,1724,1725,1726,1727,1728,1729,1730,1731,1732,1733,1734,1735,1736,1737,1738,1739,1740,1741,1742,1743,1744,1745,1746,1747,1748,1749,1750,1751,1752,1753,1754,1755,1756,1757,1758,1759,1760,1761,1762,1763,1764,1765,1766,1767,1768,1769,1770,1771,1772,1773,1774,1775,1776,1777,1778,1779,1780,1781,1782,1783,1784,1785,1786,1787,1788,1789,1790,1791,1792,1793,1794,1795,1796,1797,1798,1799,1800,1801,1802,1803,1804,1805,1806,1807,1808,1809,1810,1811,1812,1813,1814,1815,1816,1817,1818,1819,1820,1821,1822,1823,1824,1825,1826,1827,1828,1829,1830,1831,1832,1833,1834,1835,1836,1837,1838,1839,1840,1841,1842,1843,1844,1845,1846,1847,1848,1849,1850,1851,1852,1853,1854,1855,1856,1857,1858,1859,1860,1861,1862,1863,1864,1865,1866,1867,1868,1869,1870,1871,1872,1873,1874,1875,1876,1877,1878,1879,1880,1881,1882,1883,1884,1885,1886,1887,1888,1889,1890,1891,1892,1893,1894,1895,1896,1897,1898,1899,1900,1901,1902,1903,1904,1905,1906,1907,1908,1909,1910,1911,1912,1913,1914,1915,1916,1917,1918,1919,1920,1921,1922,1923,1924,1925,1926,1927,1928,1929,1930,1931,1932,1933,1934,1935,1936,1937,1938,1939,1940,1941,1942,1943,1944,1945,1946,1947,1948,1949,1950,1951,1952,1953,1954,1955,1956,1957,1958,1959,1960,1961,1962,1963,1964,1965,1966,1967,1968,1969,1970,1971,1972,1973,1974,1975,1976,1977,1978,1979,1980,1981,1982,1983,1984,1985,1986,1987,1988,1989,1990,1991,1992,1993,1994,1995,1996,1997,1998,1999,2000
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: D96703
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-314 <STO>
A:Cross-references: GB:AE005173; NID:g6553893; PIDN:ANF16559.1; GSPDB:GN00141
C:Genetics:
A:Gene: T23K23.12
A:Map position: 1

Query Match 5.28; Score 103.5; DB 2; Length 314;
Best Local Similarity 21.48; Pred. No. 0.57;
Matches 66; Conservative 42; Mismatches 99; Indels 101; Gaps 17;
Qy 24 DIKEDIPKTVESVSGSELTPEMAP--LQGLNSGNLMQFSQSVLRNMLODIOQTANTLP 81
Db 42 DVEFELAPKLPDYL-G-EYTNEMVAFRCIASLFDHVVSVTITTTTSMI----- 88
Qy 82 KLENHNGYCFSMVLDPPKSLMWYIPLNKLYIRMKAFWVDVQFKSKMP-IQPLNLR 140
Db 89 EFDSSSECEYVLQCLDE-----IPLSEL-----KPGAPGLTKWNLQ 125
Qy 141 VFLCFNDYSAFVVRCONHLSVEPLTANNAKM-----RESLLRSENPNVYCGNAGKGI 195
Db 126 PFTHKL-USLP--KCALELMIEPSCENDTVQSPCEEETLRSD-----GK-- 169
Qy 196 SERFSVWVPLN-----MSRVSRTSG---LRTOTLAFKFCVQNS----- 230
Db 170 -ENDRTPPEWDEPDLTGRTGESGFSFGADELDRNAGFRYSENGSHLSPFKIYR 228
Qy 231 CIGRKT-SLVFCLKAGDVIQGVHVI-----HVKIC--TCPKRDRIQDEROL 275
Db 229 CVNCKESGKLLFCSSDGCVEVMVHQCLDSPSPYHDAGDFYCSLCALTCPSAEVYQFQDEV 288
Qy 276 NSKKRSV 283
Db 289 AKAKRKIV 296
RESULT 15
D96703
hypothetical protein T23K23.12 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: D96703
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: D96703
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-314 <STO>
A:Cross-references: GB:AE005173; NID:g6553893; PIDN:ANF16559.1; GSPDB:GN00141
C:Genetics:
A:Gene: T23K23.12
A:Map position: 1

Search completed: November 16, 2001, 15:50:51
Job time: 2443 sec

FT DOMAIN 288 317 OLIGOMERIZATION.
 FT DOMAIN 319 336 BASIC (REPRESSION OF DNA-BINDING).
 FT DOMAIN 268 281 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT MOD_RES 341 341 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 342 AA; 37947 MW; 87EA88CFAEE333D CRC64;

Query Match 10.0%; Score 201; DB 1; Length 342;
 Best Local Similarity 27.1%; Pred. No. 2.2e-09;
 Matches 77; Conservative 53; Mismatches 112; Indels 42; Gaps 15;

QY 43 EPMAFLQGLNSGLMQFSQSVLEMMQDIQIQTANTLPKLENNHIGGYCFSVLDE--P 100
 Db 29 ESLAPGGLSSQMDWEDPETMQE--TKNVP-TAPTVPAINSY-AGEHGFNFLEFDSGT 84
 QY 101 PKSLW-MYSIPLNKLIRNMKAFNVQFKSKMPIQIPLNLRVFLCF--SNDVSAPVVRQ 157
 Db 85 AKSVTSYVSKLGLFCOLAKTTPIGVLYKEPP-QGAVIRATSVYKTEHGVVKRCP 143
 QY 158 NLSVLEPLTANNA---KMRSLRS--ENPNSVYCGNAGKGISERFSVVVPLNMSRSVT 212
 Db 144 HHQS-EDLSNKSLLIRVEGSQLAQYFEDPN-----TRHSTVTPYER---P 186
 QY 213 RSLGTRQLTARFVQNSCIG---RKETSIVFLCKACGDIVGQHVHVKICTPKRDR 269
 Db 187 QLGSEMTILLFMCNSSCMGMNRRPILTLTETTEGEVLGRCFVRVCACPGDRK 246
 QY 270 QDERQL-----NSKKRSVPAAEEDPSKVRCAIAIKTDETE 307
 Db 247 TEGNLEKSGTKTKRSAP-APDTSTAKSKSASSGEDEKE 289

RESULT 2

P53_XIPMA STANDARD; PRT; 342 AA.
 AC Q92143;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).
 GN TP53 OR P53.
 OS Xiphophorus maculatus (Southern platyfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
 OC Cyprinodontiformes; Poeciliidae; Xiphophorus.
 OX NCBI_TaxID=8083;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RIO JAMAPA / JP 163 A;
 RX MEDLINE=98326307; PubMed=9661661;
 RA Kazianis S., Gan L., Della Coletta L., Santi B., Morizot D.C.,
 RA Nairn R.S.;
 RT "Cloning and comparative sequence analysis of TP53 in xiphophorus fish
 hybrid melanoma models.";
 RL Gene 212:31-38(1998).
 RN [2]
 RP SEQUENCE OF 190-254 FROM N.A.
 RC STRAIN=RIO JAMAPA / JP 163 A;
 RA Nairn R.S.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
 CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
 CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
 CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION. IS A TRANS-
 CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
 CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
 CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
 CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
 CC BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
 CC EXPRESSION (BY SIMILARITY).
 CC -!- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: NUCLEAR.

CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF043947; AAC31134.1; -;
 DR EMBL; AF043948; AAC26190.1; -;
 DR EMBL; U34751; AAA92052.1; -;
 DR HSP; P04637; 1TSR.
 DR InterPro: IP002117; -;
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR PROSITE; PS00348; P53; 1.
 KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
 KW Nuclear protein; Phosphorylation; Apoptosis
 FT DOMAIN 1 35 TRANSCRIPTION ACTIVATION (ACIDIC).
 FT DNA_BIND 68 255 BY SIMILARITY.
 FT DOMAIN 288 317 OLIGOMERIZATION.
 FT DOMAIN 319 336 BASIC (REPRESSION OF DNA-BINDING).
 FT DOMAIN 268 281 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT MOD_RES 341 341 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 342 AA; 37957 MW; 290739636108CEA0 CRC64;

Query Match 9.9%; Score 199; DB 1; Length 342;
 Best Local Similarity 27.0%; Pred. No. 3.2e-09;

Matches 75; Conservative 52; Mismatches 109; Indels 42; Gaps 15;

QY 49 QGLNSGLMQFSQSVLEMMQDIQIQTANTLPKLENNHIGGYCFSVLDE--PPKSLW- 105
 Db 35 EGLSQNMDWEDPETMQE--TKNVP-TAPTVPAINSY-AGEHGFNFLEFDSGTAKSVTS 90
 QY 106 MYSIPLNKLIRNMKAFNVQFKSKMPIQIPLNLRVFLCF--SNDVSAPVVRQNHLSVE 163
 Db 91 TYSVKLGLFCOLAKTTPIGVLYKEPP-QGAVIRATSVYKTEHGVVKRCPHHQS-E 148
 QY 164 PLTANNA---KMRSLRS--ENPNSVYCGNAGKGISERFSVVVPLNMSRSVTRSLTR 218
 Db 149 DLSDNKSLLIRVEGSQLAQYFEDPN-----TRHSTVTPYER---POLGSEM 192
 QY 219 QTLAFVQNSCIG---RKETSIVFLCKACGDIVGQHVHVKICTPKRDRIDRQL 275
 Db 193 TILLFMCNSSCMGMNRRPILTLTETTEGEVLGRCFVRVCACPGDRKTEGSL 252
 QY 276 -----NSKKRSVPAAEEDPSKVRCAIAIKTDETE 307
 Db 253 EKSGTKTKRSAP-APDTSTAKSKSASSGEDEKE 289

RESULT 3

P73_HUMAN STANDARD; PRT; 636 AA.
 ID P73_HUMAN
 AC O15350; O15351; Q9NFK8;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE TUMOR PROTEIN P73 (P53-LIKE TRANSCRIPTION FACTOR) (P53-RELATED
 DE PROTEIN).
 GN TP73 OR P73.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
 RC TISSUE=Colon;
 RX MEDLINE=97433090; PubMed=9288759;
 RA Kaghad M., Bonnet H., Yang A., Creancier L., Biscan J.-C., Valent A.,

RA Minty A., Chalou P., Lellis J.-M., Dumont X., Ferrara P., McKeon F.,
 RA Caput D.;
 RA "Monoclonally expressed gene related to p53 at 1p36, a region
 RT frequently deleted in neuroblastoma and other human cancers.";
 RL Cell 90:809-819(1997).
 [2]
 RN SEQUENCE FROM N.A. (ISOFORM ALPHA);
 RP MEDLINE-99289209; PubMed=10362363;
 RA Yoshikawa H., Nagashima M., Khan M.A., McMenamin M.G., Hagiwara K.,
 RA Harris C.C.;
 RT "Mutational analysis of p73 and p53 in human cancer cell lines";
 RL Oncogene 18:3415-3421(1999).
 [3]
 RN SEQUENCE FROM N.A. (ISOFORM ALPHA);
 RP MEDLINE-98389621; PubMed=9721206;
 RA Mai M., Huang H., Reed C., Qian C., Smith J.S., Alderete B.,
 RA Jenkins R., Smith D.L., Liu W.;
 RT "Genomic organization and mutation analysis of p73 in
 RT oligodendrogliomas with chromosome 1 p-arm deletions";
 RL Genomics 51:359-363(1998).
 [4]
 RN SEQUENCE FROM N.A. (ISOFORMS GAMMA AND DELTA);
 RP TISSUE-Neuroblastoma;
 RX MEDLINE-99021697; PubMed=9802988;
 RA De Laurenzi V., Costanzo A., Barcaroli D., Terrinoni A., Falco M.,
 RA Annichiarico-Petruzzelli M., Leviero M., Melino G.;
 RT "Two new p73 splice variants, gamma and delta, with different
 RT transcriptional activity";
 RL J. Exp. Med. 188:1763-1768(1998).
 [5]
 RN SEQUENCE FROM N.A. (ISOFORMS EPSILON AND ZETA);
 RP TISSUE-Lymphocytes, Breast cancer, Hepatoma, and Skin;
 RX MEDLINE-99310938; PubMed=10361648;
 RA De Laurenzi V., Catani M.V., Terrinoni A., Corazzari M., Melino G.,
 RA Costanzo A., Leviero M., Knight R.A.;
 RT "Additional complexity in p73: induction by mitogens in
 RT and identification of two new splicing variants epsilon and zeta";
 RL Cell Death Differ. 6:389-390(1999).
 [6]
 RN SEQUENCE FROM N.A. (ISOFORM KAPPA);
 RP Thomas D.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 [7]
 RN PHOSPHORYLATION (ISOFORMS ALPHA AND BETA);
 RX MEDLINE-99318135; PubMed=10391251;
 RA Yuan Z.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,
 RA Kharbanda S., Weichselbaum R., Kufe D.;
 RT "p73 is regulated by tyrosine kinase c-Abl in the apoptotic response
 RT to DNA damage";
 RL Nature 399:814-817(1999).
 [8]
 RN ERRATUM;
 RA Yuan Z.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,
 RA Kharbanda S., Weichselbaum R., Kufe D.;
 RL Nature 400:792-792(1999).
 [9]
 RN FUNCTION;
 RP MEDLINE-99217940; PubMed=10203277;
 RA Kselin W.G. Jr.;
 RT "The emerging p53 gene family";
 RL J. Natl. Cancer Inst. 91:594-598(1999).
 [10]
 RN STRUCTURE BY NMR OF 439-506;
 RX MEDLINE-99380160; PubMed=1044909;
 RA Chi S.W., Ayed A., Arrowsmith C.H.;
 RT "Solution structure of a conserved C-terminal domain of p73 with
 RT structural homology to the SAM domain";
 RL EMBO J. 18:4438-4445(1999).
 [11]
 RN FUNCTION;
 CC -1- FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE.
 CC WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE
 CC PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR
 CC PROTEIN.
 CC -1- SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABL

CC TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY
 CC AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT. ISOFORM GAMMA
 CC INTERACTS HOMOTYPICALLY AND WITH ALL P73 ISOFORMS. ISOFORM DELTA
 CC INTERACTS WITH ISOFORM GAMMA, ALPHA, AND HOMOTYPICALLY.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- ALTERNATIVE PRODUCTS: 7 ISOFORMS: ALPHA (SHOWN HERE), BETA, GAMMA,
 CC DELTA, EPSILON, ZETA AND KAPPA; ARE PRODUCED BY ALTERNATIVE
 CC SPLICING. THE SPLICING OF EXON 11 IN GAMMA AND EPSILON ISOFORMS
 CC RESULTS IN A FRAMESHIFT FROM THE ORIGINAL READING FRAME. THE
 CC SPLICING OF EXON 13 IN EPSILON ISOFORM REVERTS THE READING FRAME
 CC TO THE ALPHA ISOFORM.
 CC -1- TISSUE SPECIFICITY: BRAIN, KIDNEY, PLACENTA, COLON, HEART, LIVER,
 CC SPLEEN, SKELETAL MUSCLE, PROSTATE, THYMUS AND PANCREAS.
 CC -1- INDUCTION: NOT INDUCED BY DNA DAMAGE.
 CC -1- DOMAIN: POSSESSES AN ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL DNA
 CC BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT BINDS
 CC TO THE ABL TYROSINE KINASE SH3 DOMAIN.
 CC -1- DISEASE: MAPS TO A CHROMOSOME REGION FREQUENTLY MUTATED IN DIVERSE
 CC CELL LINES OF HUMAN CANCER. APPEARS NOT TO BE FREQUENTLY MUTATED
 CC IN HUMAN CANCERS, IN CONTRAST TO P53. HEMIZYGOSITY IS OBSERVED IN
 CC NEUROBLASTOMA AND OLIGODENDROGLIOMA.
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 CC
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 CC
 CC EMBL: Y11416; CAA72220.1; -
 CC EMBL: Y11416; CAA72221.1; -
 CC EMBL: Y11416; CAA72219.1; -
 CC EMBL: AF077628; AAC61887.1; JOINED.
 CC EMBL: AF077616; AAC61887.1; JOINED.
 CC EMBL: AF077617; AAC61887.1; JOINED.
 CC EMBL: AF077618; AAC61887.1; JOINED.
 CC EMBL: AF077619; AAC61887.1; JOINED.
 CC EMBL: AF077620; AAC61887.1; JOINED.
 CC EMBL: AF077621; AAC61887.1; JOINED.
 CC EMBL: AF077624; AAC61887.1; JOINED.
 CC EMBL: AF077625; AAC61887.1; JOINED.
 CC EMBL: AF077626; AAC61887.1; JOINED.
 CC EMBL: AF077627; AAC61887.1; JOINED.
 CC EMBL: AF079094; AAD39696.1; -
 CC EMBL: AF079082; AAD39696.1; JOINED.
 CC EMBL: AF079083; AAD39696.1; JOINED.
 CC EMBL: AF079084; AAD39696.1; JOINED.
 CC EMBL: AF079085; AAD39696.1; JOINED.
 CC EMBL: AF079086; AAD39696.1; JOINED.
 CC EMBL: AF079087; AAD39696.1; JOINED.
 CC EMBL: AF079088; AAD39696.1; JOINED.
 CC EMBL: AF079089; AAD39696.1; JOINED.
 CC EMBL: AF079090; AAD39696.1; JOINED.
 CC EMBL: AF079091; AAD39696.1; JOINED.
 CC EMBL: AF079092; AAD39696.1; JOINED.
 CC EMBL: AF079093; AAD39696.1; JOINED.
 CC EMBL: ALI36528; CAB92742.1; -
 CC PDB: 1COK; 17-AUG-99.
 CC MIN: 601990; -
 CC InterPro: IPR002117; -
 CC Pfam: PF00870; P53; 1.
 CC PRINTS: PR00386; P53SUPPRESSR.
 CC PROSITE: PS00348; P53; 1.
 CC Transcription regulation: Activator; DNA-binding; Anti-oncogene;
 CC Apoptosis; Nuclear protein; Phosphorylation; Alternative splicing;
 CC 3D-structure.
 CC DOMAIN 1 46
 CC TRANSACTIVATION (BY SIMILARITY).
 CC ASP/GLU-RICH (ACIDIC).
 CC NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 CC MEDIATES OLIGOMERIZATION (POTENTIAL).
 CC POLY-PRO.
 CC DOMAIN 168 171

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FT DOMAIN 391 394 POLY-GLN.
FT DOMAIN 483 486 POLY-PRO.
FT DOMAIN 131 310 DNA-BINDING (POTENTIAL).
FT MOD_RES 99 99 PHOSPHORYLATION (BY ABL; ISOFORM BETA).
FT VARSPLIC 282 282 G -> GNRCHHWLVDGRLSPVLOGPSG (IN ISOFORM KAPPA).
FT VARSPLIC 495 636 SELTGLGPGNIEFTSQGLSQSYHLNLTIEDGALKIPE
FT VARSPLIC 400 476 QYRMITWRGLQDLAQHDYSTAQQLRNSNAATISIGSGE
FT VARSPLIC 400 403 LQORQVMEAVHFRVHTITIPNRGGPGGPDWADFGDLP
FT VARSPLIC 400 445 DCKARKQPIKEEFTAEIHH -> RTWGP (IN ISOFORM BETA).
FT VARSPLIC 477 636 SHLQPPSGPVLPSPMKVHGMMN:LPVSQNLVGGPPPHSSA
FT VARSPLIC 400 403 SHLQ -> TWGP (IN ISOFORM DELTA).
FT VARSPLIC 404 636 MISSING (IN ISOFORM DELTA).
FT VARSPLIC 400 445 SHLQPPSGPVLPSPMKVHGMMN:LPVSQNLVGGPPPHSSA
FT VARSPLIC 446 526 SHLQPPSGPVLPSPMKVHGMMN:LPVSQNLVGGPPPHSSA
FT VARSPLIC 400 495 LHSATPLRRPQPR (IN ISOFORM EPSILON).
FT VARSPLIC 400 495 MISSING (IN ISOFORM EPSILON).
FT VARSPLIC 400 495 MISSING (IN ISOFORM ZETA).
SQ SEQUENCE 636 AA; 69623 MW; A467493C5D93EEU CRC64;

```

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Query Match 9.5%; Score 191; DB 1; Length 636;
Best Local Similarity 23.9%; Pred. No. 3.5e-08;
Matches 78; Conservative 47; Mismatches 143; Indels 58; Gaps 12;

QY 17 EDDSTEVDIKEDIPKTVESGSELTPTEPMFLQGLNSGLNMQFSQSVLRMMMLQ----- 71
DB 23 EPDSTVFDLPQSSRGNNVGGTSSMDVFLHGMTYSMAQFNLLSSTMDQSSRAASA 82
QY 72 -----DIOQANTLPKLENNHTGGYCFMSWLDE---PPKSL 104
DB 83 SPYTPPEHAASVTHSPYAPQSSTFTDMSAPVIPSNTDYP-GPHHFEVTFQSSSTAKSAT 141
QY 105 WMSYIPLNKLXIRMNKAFNVDVQFKSMPIQIP-LNLRVFLCF--SNDVSAFVVRCONHLS 161
DB 142 WYSPILKLYKLCQIAK--TCPIQIKVSTPPPGTAIRAMPVYKKAHVIVDKPCPNHEL 199
QY 162 VEPLTANNAKMRESLLRSENPN-SVYCGNAQKGISERFSVWV:LNMSRSVTRSGLTRQT 220
DB 200 GRDFNEGQAPASHLIRVEGNLSQYVDDP----VTGRQSVVVPY----EPQVGTFTT 251
QY 221 LAFKFCVQNSCTIG---RKETSFLVFCLEKACGDIVGQHVHVK:CPKRDRIODE----- 272
DB 252 ILYNFMCSNCCVGGMNRRLPILITITLMDRGQVGLRRSFEGRL:CPGRDRKADEHDYRE 311
QY 273 -ROLN--SKKRKSVPEAAEEDPSKV 295
DB 312 QOALNESSAKNGAASKRAFKQSPPAV 337

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RESULT 4
ID P73_CERAE STANDARD; PRT; 637 AA.
AC Q9XK8; Q9TSQ9;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DE TUMOR PROTEIN P73 (P53-LIKE TRANSCRIPTION FACTOR) (P53-RELATED PROTEIN).
GN TP73 OR P73.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_Taxid=9534;
RN [1]
RP SEQUENCE FROM N.A.

```

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RC TISSUE=Kidney;
RA Caput D.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE.
CC WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE
CC PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR
CC PROTEIN (BY SIMILARITY).
CC -1- SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABL
CC TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY
CC AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA (SHOWN HERE) AND BETA;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- DOMAIN: POSSESSES AN ACIDIC TRANSDUCTION DOMAIN, A CENTRAL DNA
CC BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT BINDS
CC TO THE ABL TYROSINE KINASE SH3 DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC E:BL; Y11419; CAA72224.1; .
CC ER:BL; Y11419; CAA72225.1; .
CC DR HSP; P04637; LYCS.
CC DR InterPro: IPR002117; .
CC DR Pfam: PF00870; P53; 1.
CC DR PRINTS: PR00386; P53SUPPRESSR.
CC KW Transcription regulation; Activator; DNA-binding; Anti-oncogene;
CC KW Apoptosis; Nuclear protein; Phosphorylation; Alternative splicing.
CC FT VARSPLIC 495 637
CC FT QYMTIWRGLQDLAQHDYSTAQQLRNSNAATISIGSG
CC FT ELQORQVMEAVHFRVHTITIPNRGGPGGPDWADFGDLP
CC FT PCKARKQPIKEEFTAEIHH -> RTWGP (IN ISOFORM BETA).
CC SQ SEQUENCE 637 AA; 69630 MW; 7CB200B919C9C70A CRC64;

Query Match 9.5%; Score 190; DB 1; Length 637;
Best Local Similarity 23.9%; Pred. No. 4.2e-08;
Matches 78; Conservative 47; Mismatches 143; Indels 58; Gaps 12;

QY 17 EDDSTEVDIKEDIPKTVESGSELTPTEPMFLQGLNSGLNMQFSQSVLRMMMLQ----- 71
DB 23 EPDSTVFDLPQSSRGNNVGGTSSMDVFLHGMTYSMAQFNLLSSTMDQSSRAASA 82
QY 72 -----DIOQANTLPKLENNHTGGYCFMSWLDE---PPKSL 104
DB 83 SPYTPPEHAASVTHSPYAPQSSTFTDMSAPVIPSNTDYP-GPHHFEVTFQSSSTAKSAT 141
QY 105 WMSYIPLNKLXIRMNKAFNVDVQFKSMPIQIP-LNLRVFLCF--SNDVSAFVVRCONHLS 161
DB 142 WYSPILKLYKLCQIAK--TCPIQIKVSTPPPGTAIRAMPVYKKAHVIVDKPCPNHEL 199
QY 162 VEPLTANNAKMRESLLRSENPN-SVYCGNAQKGISERFSVWV:LNMSRSVTRSGLTRQT 220
DB 200 GRDFNEGQAPASHLIRVEGNLSQYVDDP----VTGRQSVVVPY----EPQVGTFTT 251
QY 221 LAFKFCVQNSCTIG---RKETSFLVFCLEKACGDIVGQHVHVK:CPKRDRIODE----- 272
DB 252 ILYNFMCSNCCVGGMNRRLPILITITLMDRGQVGLRRSFEGRL:CPGRDRKADEHDYRE 311
QY 273 -ROLN--SKKRKSVPEAAEEDPSKV 295
DB 312 QOALNESSAKNGAASKRAFKQSPPAV 337

RESULT 5
P53_CANFA

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P53_CANFA	STANDARD;	PRT;	381 AA.
ID	Q29537; G9TV78;		
AC	01-NOV-1997 (Rel. 35, Created)		
DT	15-DEC-1998 (Rel. 37, Last sequence update)		
DT	01-OCT-2000 (Rel. 40, Last annotation update)		
DE	CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).		
DE	TP53 OR P53.		
OS	Canis familiaris (Dog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.		
OX	NCBI_TaxID=9615;		
[1]	SEQUENCE FROM N.A.		
RP	TISSUE=Leukocyte;		
RX	MEDLINE=98178696; PubMed=9519881;		
RC	Veidhoen N., Milner J.;		
RT	"Isolation of canine p53 cDNA and detailed characterization of the		
RT	full length canine p53 protein.";		
RT	Oncogene 16:1077-1084(1998).		
[2]	SEQUENCE FROM N.A.		
RP	TISSUE=Spleen;		
RC	Setoguchi A., Sakai T., Okuda M., Minehata K., Yazawa M., Ishizaka T.,		
RA	Watarai T., Hasagawa A., Tsujimoto H.;		
RT	"Aberrations of p53 tumor suppressor gene in various spontaneous		
RT	tumors in the dog.";		
RT	Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.		
[3]	SEQUENCE OF 25-300 FROM N.A.		
RP	STRAIN=BEAGLE;		
RX	MEDLINE=95323915; PubMed=7600529;		
RC	Kraegel S.A., Pazzi K.A., Madewell B.R.;		
RA	"Sequence analysis of canine p53 in the region of exons 3-8.";		
RT	Cancer Lett. 92:181-186(1995).		
CC	-!- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES		
CC	GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL		
CC	CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN		
CC	TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-		
CC	ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY		
CC	CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE		
CC	ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.		
CC	APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF		
CC	BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2		
CC	EXPRESSION.		
CC	-!- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).		
CC	-!- SUBCELLULAR LOCATION: NUCLEAR.		
CC	-!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY		
CC	OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED		
CC	IN MANY TYPES OF CANCER.		
CC	-!- SIMILARITY: BELONGS TO THE P53 FAMILY.		
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CC	or send an email to license@isb-sib.ch).		
CC	EMBL; AF060514; AAC16909.1; -		
DR	EMBL; AB020761; BAA78379.1; -		
DR	EMBL; S77819; AAB42022.1; -		
DR	HSSP; P04637; LYCS.		
DR	InterPro; IPR002117; -		
DR	Pfam; PF00870; P53; 1.		
DR	PRINTS; PR00386; P53SUPPRESSR.		
DR	PROSITE; PS00348; P53; 1.		
KW	Anti-oncogene; DNA-binding; Transcription regulation; Activator;		
KW	Nuclear protein; Phosphorylation; Apoptosis.		
FT	DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).		
FT	DNA_BIND 89 280 BY SIMILARITY.		
FT	DOMAIN 313 344 OLIGOMERIZATION.		
FT	DOMAIN 356 375 BASIC (REPRESSION OF DNA-BINDING).		

QY 163 EPLTANNKMRSLRSENPVYCGNAGKGISE-----RFSVVVPLNMRSVTRSLGR 218
 Db 175 -PDSGLAPPOHLRVE-----GNLHAKYLLDRNTRFHSVVVY-----EPPEVSGDC 222
 QY 219 QTLAFKVCQNSCIG---RKETSIVFLERACDVIQGVHVKICTCPKRDRIQDERQL 275
 Db 223 TTIHFMWSSCMGNNRPIITITLSDNGKLLGRNSFEVRYCACPGDRDTEENF 282
 QY 276 NSKKRKSVPPEAAEEDPPSKVRKCAIKTDETPESNDRDCCDSDAAEWNVSRTPDGDYRLAI 335
 Db 283 RKK-----GPECPPEPGSKRALPPSTSTPPQKKKPL-----DGEY----- 320
 QY 336 TCPNKEWLOSIEGMIKEAAAEVLNPNQENLRHANKLLSLK 378
 Db 321 -----FTLQ-----INGRRFRFEMFRELNEALELK 344
 RESULT 8
 P53_PLAPE
 ID P53_PLAPE STANDARD; PRT; 366 AA.
 AC 012946;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).
 GN TP53 OR P53.
 OS Platicthys flesus (European flounder).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Pleuronectiformes;
 OC Pleuronectoidei; Pleuronectidae; Platicthys.
 OX NCBI_TaxID=8260;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99138245; PubMed=9972298;
 RA Cachot J., Gaigani F., Vincent F.;
 RT "cDNA cloning and expression analysis of flounder p53 tumour
 suppressor gene.";
 RL Comp. Biochem. Physiol. 121B:235-242(1998).
 CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
 CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
 CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
 CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-
 CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
 CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS, ONE OF THE
 CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
 CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
 CC BAX AND BAX ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
 CC EXPRESSION (BY SIMILARITY).
 CC -1- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 CC -----
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 CC -----
 DR EMBL; Y08919; CAA70123.1;
 DR HSSP; P04637; 1YGS.
 DR InterPro; IPR002117;
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR PROSITE; PS00348; P53; 1.
 KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
 KW Nuclear protein; Phosphorylation; Apoptosis.
 FT DOMAIN 1 41 TRANSCRIPTION ACTIVATION (ACIDIC).
 FT DNA_BIND 80 267 BY SIMILARITY.
 FT DOMAIN 305 336 OLIGOMERIZATION.

FT DOMAIN 341 362 BASIC (REPRESSION OF DNA-BINDING).
 FT DOMAIN 282 298 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT MOD_RES 365 365 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 366 AA; 40619 MW; 40DE4CA20B22BB88 CRC64;
 Query Match 9.0%; Score 181; DB 1; Length 366;
 Best Local Similarity 25.2%; Pred. No. 1.1e-07;
 Mismatches 80; Conservative 47; Mismatches 109; Indels 82; Gaps 15;
 QY 54 GNLMQ----FSQQSVLRMMQLQD-IOIQAANTLPKLENNHNGGYCFWSVLDE--PPKSLW- 105
 Db 44 GNLLQNGEDMNLFFELPEMVAKDSVTPPSSTVPVVDYP-GEYGFOLRFQKSGTAKSVTS 102
 QY 106 MYSIPLNKLXIRNNKAFNVVDYQFKSKMPIQLNLRVFLCP--SNVYSAPVVRQNHLSVE 163
 Db 103 TFSLLKLYCOLAKTSPEV-LLSKPPQGAIVRATAVYKTKHADVAVRCPHH----- 157
 QY 164 PLTANNAMRESLRSE--NFSVYCGNAGKGISEFVSVVVPLNMRSVTRSGLTFLA 222
 Db 158 -QTEATAEHRSHLIRLEGSORALYFEDPHTK-----RQSVTVPY-----EPQLGSETTAL 208
 QY 223 KFYVQNSCIG---RKETSIVFLERACDVIQGVHVKICTCPKRDRIQDERQ----- 274
 Db 209 LSFMCNSSCMGMMNRQILTLTLPDGLVLRRCFEVRVACVACPGDRKRDDESSTKTP 268
 QY 275 ---LNSKKRKSVP-----FAAED----- 290
 Db 269 NGPKOTKRRKQAPSNAPHTTTVMKSSSSAAEEDKEVFTVLVKGREYRIKKINEAF 328
 QY 291 -----EPKSVRRCTAIKTE 304
 Db 329 EGAREKEKAKNKVAVKQE 346
 RESULT 9
 P53_BOVIN
 ID P53_BOVIN STANDARD; PRT; 386 AA.
 AC Q29628;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).
 GN TP53.
 OS Bos taurus (Bovine), and Bos indicus (Zebu).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913, 9915;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Bovine; TISSUE=Liver;
 RX MEDLINE=9532829; PubMed=7626789;
 RA Dequiedt F., Kettmann R., Burny A., Willems L.;
 RT "Nucleotide sequence of the bovine P53 tumor-suppressor cDNA.";
 RL DNA Seq. 5:261-264(1995).
 RN [2]
 RP SEQUENCE OF 13-386 FROM N.A.
 RC SPECIES=Bovine; STRAIN=HOLSTEIN; TISSUE=Thymus;
 RX MEDLINE=96401400; PubMed=8807776;
 RA Komori H., Ishiguro N., Horiuchi M., Shinagawa M., Aida Y.;
 RT "Predominant p53 mutations in enzootic bovine leukemic cell lines.";
 RL Vet. Immunol. Immunopathol. 52:53-63(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=B. indicus; STRAIN=BORAN; TISSUE=Blood;
 RA Bishop R.R.P., Gobright E.E.I.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
 CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
 CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
 CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-
 CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY

CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
 ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
 APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
 BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
 EXPRESSION.
 -1- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).
 -1- SUBCELLULAR LOCATION: NUCLEAR.
 -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY
 OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED
 IN MANY TYPES OF CANCER.
 -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

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 EMBL; X81704; CAA57348.1; -;
 EMBL; D49825; BAA08629.1; -;
 EMBL; U74486; AAB51214.1; -;
 HSP; P04637; 1YCR.
 InterPro: IPR002117; -;
 Pfam; PF00870; P53; 1.
 PRINTS; PR00386; P53SUPPRESSR.
 PROSITE; PS00348; P53; 1.
 KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
 Nuclear protein; Phosphorylation; Apoptosis.
 FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
 FT DNA_BIND 94 285
 FT DOMAIN 318 349
 FT BASIC 361 380
 FT BASIC (REPRESSION OF DNA-BINDING).
 FT DOMAIN 304 316
 FT NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT MOD_RES 385 385
 FT PHOSPHORYLATION (BY SIMILARITY).
 FT CONFLICT 380 380 R -> T (IN REF. 2).
 SQ SEQUENCE 386 AA; 43255 MW; 222473f28c548f31 CRC64;

 Query Match 9.0%; Score 180.5; DB 1; Length 386;
 Best Local Similarity 24.7%; Pred. No. 1.3e-07;
 Matches 70; Conservative 50; Mismatches 120; Indels 43; Gaps 12;
 QY 107 YSTPLNKLVIIRNKAFFNVQVQKSKMPEIQPLNLRVFLCF--NDVAPVVRQNHLSVPEP 164
 Db 118 YPSLNLKFLCOLAKTCPVQLWDSFPP-FGRVRAMAIYKKLHMTVEVRCPPHRSDD 176
 QY 165 LTANNAKMRRESLLRSENPNSVYCGNAQKGISE----RFSVVVPLNMSRVSRTGLTRQT 220
 Db 177 YSDGLAP-PQHLIRVE-----GNLRABYLDDQNTFRHSVVVPEYSEPIDSEC---TT 224
 QY 221 LAFKVFQNSCIG---RKETSLVFLCKACGDIVGQHVHVKICTCPKRDRIQDERQLNS 277
 Db 225 IYHFNWNSCCMGGMNRRPILTIITLEDSCGNLGRNFEVRCACPGDRKTEENLR- 283
 QY 278 KKRKSVPEAAEDPSKVRCAIAKTEDTESNDSDCAAEMNVSRTPDGDY-RLAIT 336
 Db 284 KKGQSQP---EPPRSTKRALPTNT-----SSSPQPKKKPLDGEYFTLQIR 326
 QY 337 CPNKWLLQSLIEGMIKEAAEVLNRNQNLRHANKLLSLKK 379
 Db 327 GFKRYEMFRELDALELKDALDGRFEGES--RAHSSHLKSKKR 367

 RESULT 10
 P53_TETNU
 ID P53_TETNU
 AC Q9W679;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).

GN TP53 OR P53.
 OS Tetraodon milturus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=94908;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Ovary;
 RA Bhaskaran A., May D., Rand-Weaver M., Tyler C.R.;
 RT "Evolutionary conservancy of p53 gene sequences in fish."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBI databases.
 CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
 CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
 CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
 CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-
 CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
 CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
 CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
 CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
 CC BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
 CC EXPRESSION (BY SIMILARITY).
 CC -1- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

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 or send an email to license@isb-sib.ch).

 EMBL; AF071571; AAD34213.1; -;
 DR InterPro; IPR002117; -;
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR PROSITE; PS00348; P53; 1.
 KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
 Nuclear protein; Phosphorylation; Apoptosis.
 FT DOMAIN 1 47 TRANSCRIPTION ACTIVATION (ACIDIC).
 FT DNA_BIND 86 273
 FT DOMAIN 308 337
 FT BASIC (REPRESSION OF DNA-BINDING).
 FT DOMAIN 342 363
 FT NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT MOD_RES 366 366
 FT PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 367 AA; 41266 MW; ACC10BEE2F5F9CFD CRC64;

 Query Match 8.9%; Score 179; DB 1; Length 367;
 Best Local Similarity 26.8%; Pred. No. 1.6e-07;
 Matches 69; Conservative 40; Mismatches 96; Indels 52; Gaps 11;
 QY 107 YSTPLNKLVIIRNKAFFNVQVQKSKMPEIQPLNLRVFLCF--NDVAPVVRQNHLSVPEP 164
 Db 110 YSELNKLFCQAKTSLVELLLGKDPDPMGAV-LRATAIYKKTEHVAEVRRCPPHQN--- 165
 QY 165 LTANNAKMRRESLLRSE-NPNSVYCGNAQKGISEFVSVVVPLNMSRVSRTGLTRQTLAF 223
 Db 166 --EDSAEHSRLIRMEGSEARQYFEHPHYK----RQSVTVFY----EPPQLGSEFTILL 215
 QY 224 KVFQNSCIG---RKETSLVFLCKACGDIVGQHVHVKICTCPKRDRIQDERQ----- 274
 Db 216 SEMCNSSCMGMNRRPILTIITLQEGIVLGRRCFCFVRCACPGDRKTEENSTKQGN 275
 QY 275 --LNSKKRSVP-----EAAEEDPSKV-----RRCIAKTEDTESNDSR 312
 Db 276 DAKDAKKRSVPTDSTTIKKSKTASAEEDNNEVYTLQIRGRKRYEMLK---KINDGL 331
 QY 313 DCDDSAAEWNVSRTPDG 329
 | : : : : : |


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Db 332 DLLENKPKSKATHRDPG 348
RESULT 11
P53_XENLA
ID P53_XENLA STANDARD; PRT; 363 AA.
AC P07193;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).
GN TP53.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88143684; PubMed=2830576;
RA Soussi T., de Fromental C.C., Mechali M., May P., Kress M.;
RT "Cloning and characterization of a cDNA from Xenopus laevis coding
RL for a protein homologous to human and murine p53."
RL Oncogene 1:71-78(1987).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94134403; PubMed=8302570;
RA Hoever M., Clement J.H., Wedlich D., Montenarh M., Knoechel W.;
RT "Overexpression of wild-type p53 interferes with normal development
RT in Xenopus laevis embryos."
RL Oncogene 9:109-120(1994).
CC -!- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-
CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
CC BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
CC EXPRESSION (BY SIMILARITY).
CC -!- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- TISSUE SPECIFICITY: UBIQUITOUS.
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC -----
DR EMBL; M56962; AAA49923.1; -
DR EMBL; X05191; CAA28821.1; -
DR EMBL; X77546; CAA54672.1; -
DR EMBL; S68353; AAC60746.1; -
DR PIR; A29376; A29376.
DR HSP; P04637; ITR.
DR InterPro; IPR002117; -.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 29 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 76 267 BY SIMILARITY.
FT DOMAIN 300 331 OLIGOMERIZATION.
FT DOMAIN 344 356 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 281 293 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 362 362 PHOSPHORYLATION (BY SIMILARITY).
FT CONFLICT 52 52 T -> S (IN REF. 2).

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FT CONFLICT 71 71 MISSING (IN REF. 2).
FT CONFLICT 296 296 MISSING (IN REF. 2).
SQ SEQUENCE 363 AA; 40692 MW; CE1F3E58F020D74D CRC64;

Query Match
Best Local Similarity 8.8%; Score 176.5; DB 1; Length 363;
Matches 73; Conservative 46; Mismatches 119; Indels 41; Gaps 13;

QY 55 NLMQFSQSVLRMMQLDIOIQANTLPKLENNHNI-----GGYCFSWLDE--PPKSL- 104
Db 38 NLSEFPDYPLAADMVQLQGLMGNAVPTVTSCAVPSTDYAGKYQLQDFOQNGTAKSVT 97
QY 105 WMYSLPLANKLYIRNKAFFNDVQFQSKMPQLPLNLRVPLCF--SNDVSAPVVRQNH-LS 161
Db 98 CTYSELANKLCFCQAQKTCPLVRVESPPPPRSGI-LRATAVYKKSEHVAEYVWRCFPHHRS 156
QY 162 VEPLTANNKMRRESLLRSENPNVYCGNAQKGI-----SERFSVWVPLNMSRVTSRGLT 217
Db 157 VEP--GEDAAPPSHLMVE-----GNLQAYMEDVNSGRHSVCVDPY---EGPQVGTE 203
QY 218 ROTLAFKEVCONSCIG---RKETSLVFLCEKACGDIQGHVIVHKICTCPKRDRIQDERQ 274
Db 204 CTTVLYNTMNSCMGMNRRPILITITLTPOGLLLGRCCFEVRVCACPGDR-RTED 262
QY 275 LNSKKRKSVPPEAAEE-----DEPSKVRCAITKEDTE 307
Db 263 NYTKRGLKPSGKRELAAHPSPSEPLPKRRLVWVDDDEE 301

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RESULT 12
P53_PIG
ID P53_PIG STANDARD; PRT; 386 AA.
AC Q9TUB2;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).
GN TP53 OR P53.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Burr P.D., Argyle D.J., Reid S.W.J., Nasir L.;
RT "Nucleotide sequence of the pig p53 tumor suppressor cDNA."
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-
CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
CC BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
CC EXPRESSION.
CC -!- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY
CC OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED
CC IN MANY TYPES OF CANCER.
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----

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DR EMBL; AF098067; AAF04620.1; -;
 DR InterPro: IPR002117; -;
 DR Pfam: PF00870; P53; 1;
 DR PRINTS: PR00386; P53SUPPRESSOR.
 DR PROSITE: PS00348; P53; 1;
 KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
 KW Nuclear protein; Phosphorylation; Apoptosis.
 FT DOMAIN 1 45 TRANSCRIPTION ACTIVATION (ACIDIC).
 FT DNA_BIND 94 285 BY SIMILARITY.
 FT DOMAIN 318 349 OLIGOMERIZATION.
 FT DOMAIN 361 380 BASIC (REPRESSION OF DNA-BINDING).
 FT DOMAIN 304 316 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT MOD_RES 385 385 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 386 AA; 42862 MW; A4C3D8E8DF5162 LC64;

Query Match 8.88; Score 176.5; DB 1; Length 386;
 Best Local Similarity 24.88; Pred. No. 2.7e-07;
 Matches 70; Conservative 49; Mismatches 120; Indels 43; Gaps 12;

QY 107 YSIPLNKLIRMKAFNVDVQFKSMPIQLPLNLRVFLCF--SNDVSAPVVRCONHLSVPE 164
 DB 118 YSPALNKLFCQLAKTCPVQL-WNSPPPGPTRVRAMAIYKKSEYEVVRCRPHHRSDD 176
 QY 165 LTANNAKMRESLLRSENPNSVYCGNAGKGISE---RFSVVVPLNMSRSTRGLTROT 220
 DB 177 YSDGLAP-PQHLIRVE-----GNLRAEYLDNRNFRHVVVVPY---EPEVGSDDTT 224
 QY 221 LAFKFCVQNSCTG---RKETSLVFCLEKACGDIVGQHVHVKICTCPKRDRIODERQLNS 277
 DB 225 IHNFCVNSCMGMNRRPILTIITLEDASGNLLGRNSFEVRVACGCRDRTEENF-L 283
 QY 278 KRKSVPEAAEEDPSKVRRCIAIKTETESNDRCDSDSAEWNVSRTPDGDY-RLAIT 336
 DB 284 KQQSCP-----EPPGSKRALPTST-----SSSPVQKKPLDGEYFTLQIR 326
 QY 337 CPNKELWISIGMKIEAAAEVLNPNQENLRHANKLLSLK 378
 DB 327 GRERFEMFRELDALELDAQTAESGEN--RAHSSHLKSK 366

RESULT 13
 P53_MESAU
 ID P53_MESAU STANDARD; PRT; 396 AA.
 AC Q00366; P97276;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).
 GN TP53.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_Taxid=10036;
 RP [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SYRIAN; TISSUE=Kidney;
 EX MEDLINE=92210007; PubMed=1555773;
 RA Legros Y., McIntyre P., Soussi T.;
 RT "The cDNA cloning and immunological characterization of hamster p53.";
 RL Gene 112:247-250(1992).
 RP [2]
 RP SEQUENCE FROM N.A.
 RA Hou E.W., Wiseman R.;
 RL Submitted (Apr-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
 CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
 CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
 CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-
 CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
 CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
 CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.

CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
 CC BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
 CC EXPRESSION.
 CC -1- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY
 CC OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED
 CC IN MANY TYPES OF CANCER.
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 CC
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; M75144; AAA37085.1; -;
 CC EMBL; U07182; AAB41344.1; -;
 CC PIR; JH0633; JH0633.
 CC HSSP; P04637; LYCO.
 CC InterPro: IPR002117; -;
 CC Pfam: PF00870; P53; 1;
 CC PRINTS: PR00386; P53SUPPRESSOR.
 CC PROSITE: PS00348; P53; 1;
 KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
 KW Nuclear protein; Phosphorylation; Apoptosis.
 FT DOMAIN 1 45 TRANSCRIPTION ACTIVATION (ACIDIC).
 FT DNA_BIND 105 295 BY SIMILARITY.
 FT DOMAIN 328 359 OLIGOMERIZATION.
 FT DOMAIN 371 390 BASIC (REPRESSION OF DNA-BINDING).
 FT DOMAIN 314 326 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT MOD_RES 395 395 PHOSPHORYLATION (BY SIMILARITY).
 FT CONFLICT 188 188 G -> S (IN REF. 2).
 SQ SEQUENCE 396 AA; 43631 MW; 906EF02568099BE3 CRC64;

Query Match 8.78; Score 174; DB 1; Length 396;
 Best Local Similarity 24.98; Pred. No. 4.5e-07;
 Matches 70; Conservative 51; Mismatches 118; Indels 42; Gaps 12;

QY 107 YSIPLNKLIRMKAFNVDVQFKSKMP-----IQPLNLRVFLCFSDNDVSAPVVRCONHLSV 162
 DB 129 YSPALNKLFCQLAKTCPVQLWVSTPPPGPTRVRAMAIYKKLQYMTVE---VRCRPHH--E 183
 QY 163 EPLTANNAKMRESLLRSE-NPNSVYCGNAGKGISEFRFSVVPVPLNMSRSTRGLTROT 221
 DB 184 RSSGGLAPPQHLIRVEGNHAEYLDKQ----TFHVSVVVVPY-----EPPEVGSDDTTI 235
 QY 222 AFRFVQNSCTG---RKETSLVFCLEKACGDIVGQHVHVKICTCPKRDRIODERQLNSK 278
 DB 236 HYNMNCSSCMGMNRRPILTIITLEDPSGNLLGRNSFEVRICACPGDRRTEKNF-QK 294
 QY 279 KRKSVPEAAEEDPSKVRRCIAIKTETESNDRCDSDSAEWNVSRTPDGDY-RLAITC 337
 DB 295 KGEPCPEL-----PPSKAKRALPTNT-----SSSPQKRKTLDGEYFTLKIRG 337
 QY 338 PNKEWLIQSIEGMKEAAAEVLNPNQENLRHANKLLSLK 378
 DB 338 QERFKMFQELNEALELKDQAQALK--ASEDSGAHSSYLKSKK 376

RESULT 14
 P53_ICTPU
 ID P53_ICTPU STANDARD; PRT; 376 AA.
 AC Q93379;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).
 GN TP53 OR P53.
 OS Ictalurus punctatus (Channel catfish).

[illegible]

FT CONFLICT 111 111 A -> V (IN REF. 2).
 FT CONFLICT 138 138 G -> A (IN REF. 2).
 FT NON_TER 280
 SQ SEQUENCE 280 AA; 30985 MW; 040F12030B5ACEE9 CRC64;

Query Match 8.58; Score 170.5; DB 1; Length 280;
 Best Local Similarity 24.8%; Pred. No. 5.5e-07;
 Matches 54; Conservative 40; Mismatches 97; Indels 27; Gaps 8;
 QY 107 YSIPLANKLYIRMNKAFTVDQFKSMFIQPLNLRVFLCF--SNDVSAPVYVRCONHLSVEP 164
 DB 76 YSPTLNKLFQIAKTCPVOLLVSSPPP-PCTVRMAIYKKSEFTVVRCPHHERCSD 134
 QY 165 LTANNAKMRESLLRSENPNSVYCGNAGKGISE---RFSVVVPLNMSRVSRTSGLTROT 220
 DB 135 -SSDGLAPPQHLIRVE-----GNLRAEYLDNRNTRHSHVVPEY-----EPPEVGSDCIT 182
 QY 221 LAFKFCQNSCIG---RKETSIVFLEKACGDIVGQVHVHVKICTCPKRDRIQDERQLNS 277
 DB 183 IHNFMCNSSCMGMNRRPILITITLEDSSGNLLGRNSFEVRVCACPGRDRTEENFRK 242
 QY 278 KKRKSVPEAAEEDPSKVRRCIAKTEDTESNDSRDCD 315
 DB 243 KE-----EPCPEPPRSTRKRVLSNTSSSPPOKKKPLD 275

Search completed: November 16, 2001, 15:56:50
 Job time: 462 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 16, 2001, 15:49:53 ; Search time 65.26 Seconds
(without alignments)
780.531 Million cell updates/sec

Title: US-09-524-101-2

Perfect score: 2008

Sequence: 1 MYISQPMXWHKSTSDSDS.....NLRHANKLLSLKRAVELP 385

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_16.*
1: sp.archaea.*
2: sp.bacteria.*
3: sp.fungi.*
4: sp.human.*
5: sp.invertebrate.*
6: sp.mammal.*
7: sp.mhc.*
8: sp.organelle.*
9: sp.phage.*
10: sp.plant.*
11: sp.podent.*
12: sp.unclassified.*
13: sp.vertebrate.*
14: sp.virus.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2008	100.0	385	5 Q9N6D8	Q9N6D8 drosophila
2	233.5	11.6	621	5 Q9NGC7	Q9ngc7 mya arenari
3	231.5	11.5	443	5 Q9NGC8	Q9ngc8 mya arenari
4	209	10.4	564	5 Q27937	Q27937 loligo forb
5	199.5	9.9	631	11 Q9JJP2	Q9jjp2 mus musculus
6	186	9.3	448	4 Q76078	Q76078 homo sapien
7	186	9.3	471	4 Q9NPH7	Q9nph7 homo sapien
8	186	9.3	487	4 Q9H3D2	Q9h3d2 homo sapien
9	186	9.3	516	4 Q9UP27	Q9up27 homo sapien
10	186	9.3	516	4 Q9P1B7	Q9p1b7 homo sapien
11	186	9.3	555	4 Q9H3D3	Q9h3d3 homo sapien
12	186	9.3	641	4 Q9UP28	Q9up28 homo sapien
13	186	9.3	641	4 Q75195	Q75195 homo sapien
14	186	9.3	680	4 Q9UE10	Q9ue10 homo sapien
15	186	9.3	680	4 Q9H3B4	Q9h3b4 homo sapien
16	185	9.2	555	11 Q9QWZ0	Q9qwz0 mus musculus
17	185	9.2	680	11 Q88898	Q88898 mus musculus
18	183.5	9.1	281	6 Q29475	Q29475 canis famli
19	183	9.1	680	11 Q9JJP6	Q9jjp6 rattus norv

20	182	9.1	461	11 Q9QWY9	Q9qwY9 mus musculu
21	182	9.1	586	11 Q89097	Q89097 mus musculu
22	181.5	9.0	246	6 Q9TUX4	Q9tux4 canis famli
23	181	9.0	483	11 Q88897	Q88897 mus musculu
24	178	8.9	356	4 Q9UP74	Q9up74 homo sapien
25	178	8.9	389	11 Q88899	Q88899 mus musculu
26	178	8.9	393	4 Q75922	Q75922 homo sapien
27	178	8.9	416	4 Q9P1B6	Q9p1b6 homo sapien
28	178	8.9	461	4 Q9P1B5	Q9p1b5 homo sapien
29	178	8.9	461	4 Q9UP26	Q9up26 homo sapien
30	178	8.9	586	4 Q75080	Q75080 homo sapien
31	178	8.9	586	4 Q9P1B4	Q9p1b4 homo sapien
32	178	8.9	586	4 Q9UBV9	Q9ubv9 homo sapien
33	177	8.8	582	13 Q9DEC7	Q9dec7 gallus gall
34	169	8.4	641	13 Q9W6E4	Q9w6e4 barbus barb
35	168.5	8.4	390	11 Q70366	Q70366 mus musculu
36	168	8.4	501	4 Q9H3P8	Q9h3p8 homo sapien
37	167.5	8.3	205	11 Q35873	Q35873 cricetus
38	167	8.3	238	14 P89004	P89004 cricetus
39	167	8.3	286	14 P90332	P90332 mastomys na
40	167	8.3	378	14 P89002	P89002 mastomys na
41	166.5	8.3	387	6 Q9N252	Q9n252 sus scrofa
42	165	8.2	352	13 Q9PSU8	Q9psu8 oryzias lat
43	165	8.2	590	11 Q9JJP1	Q9jjp1 mus musculu
44	164	8.2	286	14 P89003	P89003 mastomys na
45	163	8.1	307	11 Q9ER40	Q9er40 mus musculu

ALIGNMENTS

RESULT 1

Q9N6D8	PRELIMINARY;	PRT;	385 AA.
ID	Q9N6D8; Q9VCR8;		
AC	Q9N6D8; Q9VCR8;		
DT	01-OCT-2000 (TRENBLrel. 15, Created)		
DT	01-OCT-2000 (TRENBLrel. 15, Last sequence update)		
DT	01-MAR-2001 (TRENBLrel. 16, Last annotation update)		
DE	TRANSCRIPTION FACTOR P53 (P53 TUMOR SUPPRESSOR-LIKE PROTEIN) (P53 PROTEIN).		
DE	P53 OR CG10873.		
GN	P53 OR CG10873.		
OS	Drosophila melanogaster (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydroidea; Drosophilidae; Drosophila.		
OX	NCBI_TaxID=7227;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20239130; PubMed=10778859;		
RA	Ollmann M., Young L.M., Di Como C.J., Karim F., Belvin M.,		
RA	Robertson S.A., Whittaker K., Demsky M., Fisher W.W., Buchman A.,		
RA	Duyk G., Friedman L., Prives C., Koczynski C.;		
RT	"Drosophila p53 is a structural and functional homolog of the tumor suppressor p53.";		
RL	Cell 101:91-101(2000).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20239131; PubMed=10778860;		
RA	Brodsky M.H., Nordstrom W., Tsang G., Kwan E., Rubin G.M.,		
RA	Abrams J.M.;		
RT	"Drosophila p53 binds a damage response element at the reaper locus.";		
RL	Cell 101:103-113(2000).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RA	Potter C.J., Xu T.;		
RT	"The identification and characterization of Drosophila melanogaster p53.";		
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20319021; PubMed=10860994;		
RA	Jin S., Martinek S., Joo W.S., Wortman J.R., Mirkovic N., Sali A.,		
RA	Yandell M.D., Pavletich N.P., Young M.W., Levine A.J.;		

RT Identification and Characterization of a p53 Homologue in Drosophila
 RL melanogaster.
 RN Proc. Natl. Acad. Sci. U.S.A. 97:7301-7306(2000).

[5]

RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE-20196006; PubMed-10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.D.G.,
 RA April J.F., Agbayani A., An H.-J., Andrews-Frannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Beriman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu F., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E.C., Spradling A.C., Stapleton M., Strong R., Sun F.,
 RA Svirskas R., Tector R., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 DR EMBL; AF263722; AAF75270.1;
 DR EMBL; AF224713; AAF40427.1;
 DR EMBL; AF224714; AAF40428.1;
 DR EMBL; AF244918; AAF61572.1;
 DR EMBL; AF250918; AAF74277.1;
 DR EMBL; AE003741; AAF56087.2;
 DR FlyBase; FBgn0039044; p53.
 DR InterPro; IPR002117;
 DR PRINTS; PR00386; P53SUPPRESSR.
 SQ SEQUENCE 385 AA; 43653 MW; 8389C8FE9B8E6369 CRC64;

Query Match 100.0%; Score 2008; DB 5; Length 385;
 Best Local Similarity 100.0%; Pred. No. 1.le-168;
 Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYISQPSMHKSTSDSDSDTEVDIKEDIPKTVESGSELITPEMAFIQGLNSGNLMQFS 60
 DB 1 MYISQPSMHKSTSDSDSDTEVDIKEDIPKTVESGSELITPEMAFIQGLNS'NLMQFS 60
 QY 61 QQSVLREMLQDIQIQAANTLPKLENNHIGGYCFSWLVDPEPKSLWYKSLPKLKYLRMKN 120
 DB 61 QQSVLREMLQDIQIQAANTLPKLENNHIGGYCFSWLVDPEPKSLWYKSLPKLKYLRMKN 120
 QY 121 AFNVDFQKSMPIQPLNLRVFLCFSDNDVSAPVVRQNHLSVEPLTANNAKMRESLLRSE 180
 DB 121 AFNVDFQKSMPIQPLNLRVFLCFSDNDVSAPVVRQNHLSVEPLTANNAKMRESLLRSE 180

QY 181 NPNSVYCGNAGKGI SERFSVVVPLNMSRVSRTSLGTLROTTLAFKFCVQNSCIGRKETSIV 240
 DB 181 NPNSVYCGNAGKGI SERFSVVVPLNMSRVSRTSLGTLROTTLAFKFCVQNSCIGRKETSIV 240
 QY 241 FCLEKACGDIVGQHVHVICTCPKRDRIQDERQLNSKKRSVPEAAEEDPSKVRRCIA 300
 DB 241 FCLEKACGDIVGQHVHVICTCPKRDRIQDERQLNSKKRSVPEAAEEDPSKVRRCIA 300
 QY 301 IKTEDESNSRCDSDSAEAWNVSTPDGYRLAITCPNKEWLLQSIGMIKEAAAEVLR 360
 DB 301 IKTEDESNSRCDSDSAEAWNVSTPDGYRLAITCPNKEWLLQSIGMIKEAAAEVLR 360
 QY 361 NPNQENLRHANKLLSLKKRAYELP 385
 DB 361 NPNQENLRHANKLLSLKKRAYELP 385
 RESULT 2
 Q9NGC7
 ID Q9NGC7 PRELIMINARY; PRT; 621 AA.
 AC Q9NGC7;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE P73-Like PROTEIN.
 OS Mya arenaria.
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Myoida;
 OC Myoidae; Myidae; Mya.
 OX NCBI_TaxID:6604;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUP-GILL;
 RA Kelley M.L., Heaney J.D., Winge P., Van Beneden R.J., Walker C.W.;
 RT "Conserved p53/p73 homologs are differentially expressed in a
 RT naturally occurring invertebrate leukemia."
 RT Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF253324; AAF67734.1;
 DR InterPro; IPR001660;
 DR InterPro; IPR002117;
 DR Pfam; PF00536; SAM; 1.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR ProDom; PD002691; 1.
 SQ SEQUENCE 621 AA; 69244 MW; AB1F0C66E0010AED CRC64;

Query Match 11.6%; Score 233.5; DB 5; Length 621;
 Best Local Similarity 27.2%; Pred. No. 3e-12;
 Matches 99; Conservative 50; Mismatches 138; Indels 77; Gaps 18;

QY 4 SQPS-----WH--KSTDSED----DSTEVDIKEDIPKTVESGSELITTE-----43
 DB 20 NQPSQTFEYLWHITLVEEVDNDYTHINTRELDYSYDSE-----DGTSLQVKEFRINQH 75
 QY 44 -----PMAFLOGLSGNLMQFSQ-----SVLRMML-----QDIOIQANT 79
 DB 76 HTDVSDELNFIIGTSTSSSPDSQTNISGSTASSPYQEMALITSPPTSPHTNITSIPT 135
 QY 80 LPKLENINIGGYCFSWLDEPK-----SLMWYSLPKLYIRNKAFAFNVDFQKSK-KMPI 134
 DB 136 VPSNTNYP-GDYGFESFATPSKETKSTWTYSILKLYVRM--ATTCPVREKTLQPP 192
 QY 135 QPLNLRVFLCF--SNDVSAPVVRQNHLSVEPLTANNAKMRESLLRSNPNSVYCGNAQ 192
 DB 193 PCGVIRSMPIFKPEHVQAVKRCNPATSKFENENHPAPNH-LVRCHEKYSKYVEDP-- 249
 QY 193 KGISERFSVVVPLNMSRVSRTSLGTLROTTLAFKFCVQNSCIG---RKETSLVFCLEKACGD 249
 DB 250 --YNRQSVLIP-----QETPQAGSEWNTNLFQWCLGSCVGGPNRPLOIVTLEKD-NQ 302
 QY 250 IVGQHVHVICTCPKRDRIQDER-----QLNSKKRSVPEAAEEDPSKVRRCIAIKT 303
 DB 303 VLGRRCVEVRICACPGRKADKRGSLPPVSGVKKSQMPKFSMGTEITTVSSGKKRKF 362

[illegible]

DR EMBL; AF116763; AAF43489.1; JOINED.
 DR EMBL; AF116764; AAF43489.1; JOINED.
 DR EMBL; AF116765; AAF43489.1; JOINED.
 DR EMBL; AF116766; AAF43489.1; JOINED.
 DR InterPro: IPR002117; .
 DR Pfam: PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR PROSITE; P500348; P53; UNKNOWN_1.
 SQ SEQUENCE 471 AA; 52882 MW; 32EB39798FCICE69 CRC64;

Query Match 9.3%; Score 186; DB 4; Length 471;
 Best Local Similarity 22.2%; Pred. No. 3.2e-08;
 Matches 75; Conservative 59; Mismatches 124; Indels 80; Gaps 15;

QY 5 QPMWHEKSTDESDST-EVDIKEDIPKTVESGSLTEPMAFLQGLNSGLNQFSSQS 63
 Db 31 QPDLNFVDEPSDGTAKNIEISMD---CIRMQSDSL-SDPM-----WPQYINLG 76
 QY 64 VLREMLQDIQIQ---ANTLPKLENH-----NI 88
 Db 77 LLNSM---DQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSTFDALSPSPAIPSTNDYP 133
 QY 89 GGYCFSEWLDE---PKSLWYSLPLNKLIRNMKAFNVDVQFCKMPIOPLNLRVFLCF 145
 Db 134 GPHSFDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPP-QGAVIRAMPVY 192
 QY 146 --SNDVSAPVVRCONHLSVEPLTANNAKMRSLRSNPNSVYCGNAQKGISE----RF 199
 Db 193 KKAHEVTEVVKRCPNHLSREFNEGQIAPPSHLIRVE-----GNSHAQYVEDPITGRQ 245
 QY 200 SVVYPLNMSRSTRGLRQTLAFKVFQNSCIG---RKETSLVFCLEKACGDIVGQHV 256
 Db 246 SVLVPI---EPQVGTETTVLYNFMCNCSVCGMNRRLIIVTLETRDQGVILGRCF 301
 QY 257 HVKICTCPKRDRIQDEROLNKKRSVPEAAEDEFPSK 294
 Db 302 EARICACPGDRKRADE---DSIRKQVSDSTKNGDGTK 336

RESULT 8
 Q9H3D2 PRELIMINARY; PRT; 487 AA.
 AC Q9H3D2;
 DT 01-MAR-2001 (TREMELrel. 16, Created)
 DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)
 DE TA P63 GAMMA.
 GN P63.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98448095; PubMed=9774969;
 RA Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
 RA Andrews N.C., Caput D., McKeon F.;
 RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
 RT transactivating, death-inducing, and dominant-negative activities.";
 RL Mol. Cell 2:305-316(1998).
 DR EMBL; AF075432; AAC62637.1; .
 DR HSSP; P04637; 1YCS.
 DR InterPro; IPR002117; .
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR PRODOM; PD002681; .; 1.
 SQ SEQUENCE 516 AA; 57697 MW; 0755378C104738B1 CRC64;

Query Match 9.3%; Score 186; DB 4; Length 516;
 Best Local Similarity 22.2%; Pred. No. 3.5e-08;
 Matches 75; Conservative 59; Mismatches 124; Indels 80; Gaps 15;

QY 5 QPMWHEKSTDESDST-EVDIKEDIPKTVESGSLTEPMAFLQGLNSGLNQFSSQS 63
 Db 31 QPDLNFVDEPSDGTAKNIEISMD---CIRMQSDSL-SDPM-----WPQYINLG 76
 QY 64 VLREMLQDIQIQ---ANTLPKLENH-----NI 88
 Db 77 LLNSM---DQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSTFDALSPSPAIPSTNDYP 133
 QY 89 GGYCFSEWLDE---PKSLWYSLPLNKLIRNMKAFNVDVQFCKMPIOPLNLRVFLCF 145
 Db 134 GPHSFDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPP-QGAVIRAMPVY 192
 QY 146 --SNDVSAPVVRCONHLSVEPLTANNAKMRSLRSNPNSVYCGNAQKGISE----RF 199
 Db 193 KKAHEVTEVVKRCPNHLSREFNEGQIAPPSHLIRVE-----GNSHAQYVEDPITGRQ 245
 QY 200 SVVYPLNMSRSTRGLRQTLAFKVFQNSCIG---RKETSLVFCLEKACGDIVGQHV 256
 Db 246 SVLVPI---EPQVGTETTVLYNFMCNCSVCGMNRRLIIVTLETRDQGVILGRCF 301
 QY 257 HVKICTCPKRDRIQDEROLNKKRSVPEAAEDEFPSK 294
 Db 302 EARICACPGDRKRADE---DSIRKQVSDSTKNGDGTK 336

SQ SEQUENCE 487 AA; 55687 MW; 86CC865BDF2643DD CRC64;

Query Match 9.3%; Score 186; DB 4; Length 487;
 Best Local Similarity 22.2%; Pred. No. 3.3e-08;
 Matches 75; Conservative 59; Mismatches 124; Indels 80; Gaps 15;

QY 5 QPMWHEKSTDESDST-EVDIKEDIPKTVESGSLTEPMAFLQGLNSGLNQFSSQS 63
 Db 70 QPDLNFVDEPSDGTAKNIEISMD---CIRMQSDSL-SDPM-----WPQYINLG 115
 QY 64 VLREMLQDIQIQ---ANTLPKLENH-----NI 88
 Db 116 LLNSM---DQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSTFDALSPSPAIPSTNDYP 172
 QY 89 GGYCFSEWLDE---PKSLWYSLPLNKLIRNMKAFNVDVQFCKMPIOPLNLRVFLCF 145
 Db 173 GPHSFDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPP-QGAVIRAMPVY 231
 QY 146 --SNDVSAPVVRCONHLSVEPLTANNAKMRSLRSNPNSVYCGNAQKGISE----RF 199
 Db 232 KKAHEVTEVVKRCPNHLSREFNEGQIAPPSHLIRVE-----GNSHAQYVEDPITGRQ 284
 QY 200 SVVYPLNMSRSTRGLRQTLAFKVFQNSCIG---RKETSLVFCLEKACGDIVGQHV 256
 Db 285 SVLVPI---EPQVGTETTVLYNFMCNCSVCGMNRRLIIVTLETRDQGVILGRCF 340
 QY 257 HVKICTCPKRDRIQDEROLNKKRSVPEAAEDEFPSK 294
 Db 341 EARICACPGDRKRADE---DSIRKQVSDSTKNGDGTK 375

RESULT 9
 Q9UP27 PRELIMINARY; PRT; 516 AA.
 AC Q9UP27;
 DT 01-MAY-2000 (Tri-BLrel. 13, Created)
 DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)
 DE TA P63 BETA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98448095; PubMed=9774969;
 RA Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
 RA Andrews N.C., Caput D., McKeon F.;
 RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
 RT transactivating, death-inducing, and dominant-negative activities.";
 RL Mol. Cell 2:305-316(1998).
 DR EMBL; AF075432; AAC62637.1; .
 DR HSSP; P04637; 1YCS.
 DR InterPro; IPR002117; .
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR PRODOM; PD002681; .; 1.
 SQ SEQUENCE 516 AA; 57697 MW; 0755378C104738B1 CRC64;

Query Match 9.3%; Score 186; DB 4; Length 516;
 Best Local Similarity 22.2%; Pred. No. 3.5e-08;
 Matches 75; Conservative 59; Mismatches 124; Indels 80; Gaps 15;

QY 5 QPMWHEKSTDESDST-EVDIKEDIPKTVESGSLTEPMAFLQGLNSGLNQFSSQS 63
 Db 31 QPDLNFVDEPSDGTAKNIEISMD---CIRMQSDSL-SDPM-----WPQYINLG 76
 QY 64 VLREMLQDIQIQ---ANTLPKLENH-----NI 88
 Db 77 LLNSM---DQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSTFDALSPSPAIPSTNDYP 133

AC Q9UE10;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE KET PROTEIN.
GN KET.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SKELETAL MUSCLE AND KERATINOCYTE CULTURE;
RX MEDLINE-99018225; PubMed-9799841;
RA Augustin M., Bamberger C., Paul D., Schmale H.;
RT *Cloning and chromosomal mapping of the human p53-related KET gene to
RT chromosome 3q27 and its murine homolog Ket to mouse chromosome 16.";
RL Mamm. Genome 9:899-902(1998).
DR EMBL; Y16961; CAA76562.1; -.
DR HSSP; P04637; LYCS.
DR InterPro; IPR001660; -.
DR InterPro; IPR002117; -.
DR Pfam; PF00870; P53; 1.
DR PRINTS; P00386; P53SUPPRESSR.
DR ProDom; PD002681; 1.
DR SMART; SM00454; SAM; 1.
SQ SEQUENCE 680 AA; 76776 MW; 6548A6F2187D852E CRC64;

Query Match 9.3%; Score 186; DB 4; Length 680;
Best Local Similarity 22.2%; Pred. No. 5e-08;
Matches 75; Conservative 59; Mismatches 124; Indels 80; Gaps 15;
QY 5 QPMSNHKESTDESDST-EVDIKEDIPKTVYVSGSELTEPMAFLQGLNSGNLMQFSQOS 63
DB 70 QPDLNFVDEPSEDGATNKIEISMD--CIRMQSDSL-SDPM-----WPQYTNLG 115
QY 64 VLEEMMLQDIQI--ANTLPKLENH-----NI 88
DB 116 LLNSM--DQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPALPSNTDYP 172
QY 89 GGYCFSWLDE---PPKSLMWYSIPLNKLIRNKAFFNVDFQKSKMPIQPLNLRVFLCF 145
DB 173 GPHSFDFVSFQSSSTAKSATWTYSTELAKLYCQIAKTCPIQIKVM---PP-OGAVIRAMPVY 231
QY 146 --SNDYSAPVRCQNHLSVEPLTANNAKMRESLLRSENPNSVY--GNAQKGISE----RF 199
DB 232 KKAHEVTEVVKRCPNHLSREFNEGQIAPPSHLIRVE-----GNSHAQYVEDPITGRQ 284
QY 200 SVVPLNMSRSVTRSGLTROTIAFKFVQNSCIG---RKETSICLEKACGDIVGQHV 256
DB 285 SVLVYPY---EPPQVGTEFTVLNFMCSVCVGMNRRPILITLETRDQGVLRGRCF 340
QY 257 HVKICTCPKRDRIQDQRLNSKKRSVPEAAEEDPSK 294
DB 341 EARICACPGDRKADE--DSIRKQOVSDSTKNGDGTK 375

RESULT 15
Q9H3D4 PRELIMINARY; PRT; 680 AA.
AC Q9H3D4;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE TA P63 ALPHA.
GN P63.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE-98448095; PubMed-9774969;
RA Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
RT Andrews N.C., Caput D., McKeon F.;
RT *p53, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Hagiwara K., McMenamin M.G., Harris C.C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF124539; AAG45607.1; JOINED.
DR EMBL; AF124528; AAG45607.1; JOINED.
DR EMBL; AF124529; AAG45607.1; JOINED.
DR EMBL; AF124531; AAG45607.1; JOINED.
DR EMBL; AF124532; AAG45607.1; JOINED.
DR EMBL; AF124533; AAG45607.1; JOINED.
DR EMBL; AF124534; AAG45607.1; JOINED.
DR EMBL; AF124535; AAG45607.1; JOINED.
DR EMBL; AF124536; AAG45607.1; JOINED.
DR EMBL; AF124537; AAG45607.1; JOINED.
DR EMBL; AF124538; AAG45607.1; JOINED.
SQ SEQUENCE 680 AA; 76785 MW; F66ECD45E87D9799 CRC64;

Query Match 9.3%; Score 186; DB 4; Length 680;
Best Local Similarity 22.2%; Pred. No. 5e-08;
Matches 75; Conservative 59; Mismatches 124; Indels 80; Gaps 15;
QY 5 QPMSNHKESTDESDST-EVDIKEDIPKTVYVSGSELTEPMAFLQGLNSGNLMQFSQOS 63
DB 70 QPDLNFVDEPSEDGATNKIEISMD--CIRMQSDSL-SDPM-----WPQYTNLG 115
QY 64 VLEEMMLQDIQI--ANTLPKLENH-----NI 88
DB 116 LLNSM--DQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPALPSNTDYP 172
QY 89 GGYCFSWLDE---PPKSLMWYSIPLNKLIRNKAFFNVDFQKSKMPIQPLNLRVFLCF 145
DB 173 GPHSFDFVSFQSSSTAKSATWTYSTELAKLYCQIAKTCPIQIKVM---PP-OGAVIRAMPVY 231
QY 146 --SNDYSAPVRCQNHLSVEPLTANNAKMRESLLRSENPNSVY--GNAQKGISE----RF 199
DB 232 KKAHEVTEVVKRCPNHLSREFNEGQIAPPSHLIRVE-----GNSHAQYVEDPITGRQ 284
QY 200 SVVPLNMSRSVTRSGLTROTIAFKFVQNSCIG---RKETSICLEKACGDIVGQHV 256
DB 285 SVLVYPY---EPPQVGTEFTVLNFMCSVCVGMNRRPILITLETRDQGVLRGRCF 340
QY 257 HVKICTCPKRDRIQDQRLNSKKRSVPEAAEEDPSK 294
DB 341 EARICACPGDRKADE--DSIRKQOVSDSTKNGDGTK 375

Search completed: November 16, 2001, 15:58:09
Job time: 496 sec

